



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : C12N 9/88, C12P 19/02	A2	(11) International Publication Number: <b>WO 98/50532</b> (43) International Publication Date: 12 November 1998 (12.11.98)
<p>(21) International Application Number: PCT/IB98/00708</p> <p>(22) International Filing Date: 6 May 1998 (06.05.98)</p> <p>(30) Priority Data: 9709161.5 6 May 1997 (06.05.97) GB</p> <p>(71) Applicant (for all designated States except US): DANISCO A/S [DK/DK]; Langebrogade 1, P.O. Box 17, DK-1001 Copenhagen K (DK).</p> <p>(72) Inventors; and (75) Inventors/Applicants (for US only): BUCHTER-LARSEN, Aksel [DK/DK]; Amager Felledves 27, DK-2300 Copenhagen (DK). MARCUSSEN, Ian [DK/DK]; Knabrostrede 25, DK-1210 Copenhagen (DK).</p> <p>(74) Agents: HARDING, Charles, Thomas et al.; D. Young &amp; Co., 21 New Fetter Lane, London EC4A 1DA (GB).</p>	<p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p><b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i></p>	
(54) Title: A PROCESS FOR PREPARING AN ANTI-OXIDANT		
<p>(57) Abstract</p> <p>A process of preparing an anti-oxidant is described. The process comprises preparing a medium that comprises an anti-oxidant and at least one other component. The process comprises preparing <i>in situ</i> in the medium the anti-oxidant. The anti-oxidant is prepared from either a glucan by use of recombinant DNA techniques and/or by use of a recombinant glucan lyase.</p>		

*FOR THE PURPOSES OF INFORMATION ONLY*

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LJ	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

## A PROCESS OF PREPARING AN ANTI-OXIDANT

The present invention relates to a process of preparing an anti-oxidant.

5 An anti-oxidant prevents, inhibits or reduces the oxidation rate of an oxidisable medium. In particular, anti-oxidants are used for the preservation of food, especially when the food is or comprises a fat. Typical chemical anti-oxidants include aromatic amines, substituted phenols and sulphur compounds. Examples of anti-oxidants for food products are polyvinylpolypyrrolidone, dithiothreitol, sulphur dioxide, synthetic  
10  $\gamma$ -tocopherol,  $\delta$ -tocopherol, L-ascorbic acid, sodium L-ascorbate, calcium L-ascorbate, ascorbyl palmitate, propyl gallate, octyl gallate, dodecyl gallate, lecithin, diphenylamine ethoxyquin and butylated hydroxytoluene. Two commonly used anti-oxidants are GRINDOX 142 (obtained from Danisco A/S) and GRINDOX 1029 (obtained from Danisco A/S).

15

Typically, anti-oxidants are added to foodstuffs, such as beverages.

For example, anti-oxidants are used in the preparation of alcoholic beverages such as beer, cider, ale etc.. In particular, there is a wide spread use of anti-oxidants in the  
20 preparation of wine. In this regard, Butzke and Bisson in *Agro-Food-Industry Hi-Tech* (July/August 1996 pages 26-30) present a review of wine manufacture.

According to Butzke and Bisson (*ibid*):

25 *"Wine is the product of the natural fermentation of grape must or juice. In the case of red wine, the skins are present during the initial fermentation to allow extraction of pigment and important flavour and aroma constituents from the skin. The term "must" refers to the crushed whole grapes. In the case of white wine production, skins are  
30 removed prior to fermentation and only the juice is retained and processed. ....*

5       *Grapes are harvested and brought directly to the winery from the field. The grapes are then crushed at the winery and the must either transferred to a tank for fermentation (red wine) or pressed to separate juice from the skin and seeds (white wine). In this latter case, the*  
10       *juice is then transferred to a tank for fermentation. The tanks may either be inoculated with a commercial wine strain of Saccharomyces or allowed to undergo a natural or uninoculated fermentation. In a natural fermentation, Saccharomyces cells are greatly outnumbered by wild (non-Saccharomyces) yeast and bacteria at the beginning of*  
15       *fermentation. By the end of the fermentation Saccharomyces is the dominant and most often only organism isolateable. Inoculation with a commercial wine strain or with fermenting juice or must changes the initial ratio of the numbers of different microorganisms, allowing Saccharomyces to dominate the fermentation much earlier.*

20       *The metabolic activity of microorganisms in wine results in the production of aroma and flavour compounds some of which are highly objectionable to the consumer and all of which are distinct from the compounds responsible for the varietal character of the wine. ....*  
25       *Sulphur dioxide addition prevents chemical oxidation reactions and in this sense is an important stabilizer of the natural grape aroma and flavour. It may be added to the must or juice to preserve flavour, not necessarily as an antimicrobial agent. However, its antimicrobial activity must be considered when choosing a strain to be genetically modified for wine production."*

Hence, potentially harmful chemicals - such as sulphur dioxide - are used in wine manufacture.

30       The present invention seeks to overcome any problems associated with the prior art methods of preparing foodstuffs with antioxidants.

According to a first aspect of the present invention there is provided a process of preparing a medium that comprises an anti-oxidant and at least one other component, the process comprising preparing *in situ* in the medium the anti-oxidant; and wherein the anti-oxidant is prepared from a glucan by use of recombinant DNA techniques.

5

According to a second aspect of the present invention there is provided a process of preparing a medium that comprises an anti-oxidant and at least one other component, the process comprising preparing *in situ* in the medium the anti-oxidant; and wherein the anti-oxidant is prepared by use of a recombinant glucan lyase.

10

According to a third aspect of the present invention there is provided a medium prepared by the process according to the present invention.

Other aspects of the present invention include:

15

Use of anhydrofructose as an anti-oxidant for a medium comprising at least one other component, wherein the anhydrofructose is prepared *in situ* in the medium.

20

Use of anhydrofructose as a means for imparting or improving stress tolerance in a plant, wherein the anhydrofructose is prepared *in situ* in the plant.

25

Use of anhydrofructose as a means for imparting or improving the transformation of a grape, wherein the anhydrofructose is prepared *in situ* in the grape.

30

Use of anhydrofructose as a means for increasing antioxidant levels in a foodstuff (preferably a fruit or vegetable, more preferably a fresh fruit or a fresh vegetable), wherein the anhydrofructose is prepared *in situ* in the foodstuff.

Use of anhydrofructose as a pharmaceutical in a foodstuff, wherein the anhydrofructose is prepared *in situ* in the foodstuff.

5 A method of administering a foodstuff comprising anhydrofructose, wherein the anhydrofructose is in a pharmaceutically acceptable amount and acts as a pharmaceutical; and wherein the anhydrofructose has been prepared *in situ* in the foodstuff.

10 Use of anhydrofructose as a nutraceutical in a foodstuff, wherein the anhydrofructose is prepared *in situ* in the foodstuff.

15 A method of administering a foodstuff comprising anhydrofructose, wherein the anhydrofructose is in a nutraceutically acceptable amount and acts as a nutraceutical; and wherein the anhydrofructose has been prepared *in situ* in the foodstuff.

Use of glucan lyase as a means for imparting or improving stress tolerance in a plant, wherein the glucan lyase is prepared *in situ* in the plant.

20 Use of glucan lyase as a means for imparting or improving the transformation of a grape, wherein the glucan lyase is prepared *in situ* in the grape.

25 Use of glucan lyase as a means for increasing antioxidant levels in a foodstuff (preferably a fruit or vegetable, more preferably a fresh fruit or a fresh vegetable), wherein the glucan lyase is prepared *in situ* in the foodstuff.

Use of glucan lyase in the preparation of a pharmaceutical in a foodstuff, wherein the glucan lyase is prepared *in situ* in the foodstuff.

30 A method of administering a foodstuff comprising an antioxidant, wherein the antioxidant is in a pharmaceutically acceptable amount and acts as a pharmaceutical; and wherein the antioxidant has been prepared *in situ* in the

foodstuff from a glucan lyase.

Use of glucan lyase in the preparation of a nutraceutical in a foodstuff, wherein the glucan lyase is prepared *in situ* in the foodstuff.

5

A method of administering a foodstuff comprising an antioxidant, wherein the antioxidant is in a nutraceutically acceptable amount and acts as a nutraceutical; and wherein the antioxidant has been prepared *in situ* in the foodstuff from a glucan lyase.

10

Use of a nucleotide sequence coding for a glucan lyase as a means for imparting or improving stress tolerance in a plant, wherein the nucleotide sequence is expressed *in situ* in the plant.

15

Use of a nucleotide sequence coding for a glucan lyase as a means for imparting or improving the transformation of a grape, wherein the nucleotide sequence is expressed *in situ* in the grape.

20

Use of a nucleotide sequence coding for a glucan lyase as a means for increasing antioxidant levels in a foodstuff (preferably a fruit or vegetable, more preferably a fresh fruit or a fresh vegetable), wherein the nucleotide sequence is expressed *in situ* in the foodstuff.

25

Use of a nucleotide sequence coding for a glucan lyase as a means for creating a pharmaceutical in a foodstuff, wherein the nucleotide sequence is expressed *in situ* in the foodstuff.

30

A method of administering a foodstuff comprising an antioxidant, wherein the antioxidant is in a pharmaceutically acceptable amount and acts as a pharmaceutical; and wherein the antioxidant has been prepared *in situ* in the foodstuff by means of a nucleotide sequence coding for a glucan lyase.

Use of a nucleotide sequence coding for a glucan lyase as a means for creating a nutraceutical in a foodstuff, wherein the nucleotide sequence is expressed *in situ* in the foodstuff.

5 A method of administering a foodstuff comprising an antioxidant, wherein the antioxidant is in a nutraceutically acceptable amount and acts as a nutraceutical; and wherein the antioxidant has been prepared *in situ* in the foodstuff by means of a nucleotide sequence coding for a glucan lyase.

10 The term "nutraceutical" means a compound that is capable of acting as a nutrient (i.e. it is suitable for, for example, oral administration) as well as being capable of exhibiting a pharmaceutical effect and/or cosmetic effect.

In contrast to the usual practice of adding anti-oxidants media, such as foodstuffs, we  
15 have now found that particular anti-oxidants can be prepared *in situ* in the medium.

The *in situ* preparation of anti-oxidants is particularly advantageous in that less, or even no, additional anti-oxidants need be added to the medium, such as a food product.

20 The present invention is also believed to be advantageous as it provides a means of improving stress tolerance of plants.

The present invention is also advantageous as it provides a means for viably  
25 transforming grape.

The present invention is further advantageous in that it enables the levels of antioxidants in foodstuffs to be elevated. This may have beneficial health implications. In this regard, recent reports (e.g. Biotechnology Newswatch April 21  
30 1997 "Potent Antioxidants, as strong as those in fruit, found in coffee" by Marjorie Shaffer) suggest that antioxidants have a pharmaceutical benefit, for example in preventing or suppressing cancer formation.



General *in situ* preparation of antioxidants in plants has been previously reviewed by Badiani *et al* in *Agro-Food-Industry Hi-Tech* (March/April 1996 pages 21-26). It is to be noted, however, that this review does not mention preparing *in situ* antioxidants from a glucan, let alone by use of a recombinant glucan lyase.

5

Preferably, the glucan comprises  $\alpha$ -1,4 links.

Preferably, the glucan is starch or a unit of starch.

10 Preferably, the glucan is a substrate for a recombinant enzyme such that contact of the glucan with the recombinant enzyme yields the anti-oxidant.

Preferably, the enzyme is a glucan lyase.

15 Preferably, the enzyme is an  $\alpha$ -1,4-glucan lyase.

Preferably, the enzyme comprises any one of the sequences shown as SEQ ID Nos 1-6, or a variant, homologue or fragment thereof.

20 Preferably, the enzyme is any one of the sequences shown as SEQ ID Nos 1-6.

Preferably, the enzyme is encoded by a nucleotide sequence comprising any one of the sequences shown as SEQ ID Nos 7-12, or a variant, homologue or fragment thereof.

25

Preferably, the enzyme is encoded by a nucleotide sequence having any one of the sequences shown as SEQ ID Nos 7-12.

Preferably, the anti-oxidant is anhydrofructose.

30

Preferably, the anti-oxidant is 1,5-D-anhydrofructose.

Preferably, the-medium is, or is used in the preparation of, a foodstuff.

Preferably, the foodstuff is a beverage.

5 Preferably, the beverage is an alcoholic beverage.

Preferably, the beverage is a wine.

10 Preferably, the anti-oxidant is prepared *in situ* in the component and is then released into the medium.

Preferably, the component is a plant or a part thereof.

15 Preferably, the component is all or part of a cereal or a fruit.

Preferably, the component is all or part of a grape.

20 The medium may be used as or in the preparation of a foodstuff, which includes beverages. In the alternative, the medium may be for use in polymer chemistry. In this regard, the *in situ* generated anti-oxidants could therefore act as oxygen scavengers during, for example, the synthesis of polymers, such as the synthesis of bio-degradable plastic.

25 In accordance with the present invention, the anti-oxidant (preferably anhydrofructose) is prepared *in situ* in the medium. In other words, the antioxidant (preferably anhydrofructose) that is prepared *in situ* in the medium is used as an anti-oxidant in the medium. In one embodiment, the antioxidant (preferably anhydrofructose) that is prepared *in situ* in the medium is used as the main anti-oxidant in the medium.

30 The term "*in situ* in the medium" as used herein includes the anti-oxidant being prepared by action of a recombinant enzyme expressed by the component on a glucan - which glucan is a substrate for the enzyme. The term also includes the anti-oxidant

being prepared by action of a recombinant enzyme expressed by the component on a glucan - which glucan is a substrate for the enzyme - within the component and the subsequent generation of the anti-oxidant. The term also includes the recombinant enzyme being expressed by the component and then being released into the medium, which enzyme acts on a glucan - which glucan is a substrate for the enzyme - present in the medium to form the anti-oxidant in the medium. The term also covers the presence or addition of another component to the medium, which component then expresses a recombinant nucleotide sequence which results in exposure of part or all of the medium to an anti-oxidant, which anti-oxidant may be a recombinant enzyme or a recombinant protein expressed and released by the other component, or it may be a product of a glucan - which glucan is a substrate for the enzyme - within the medium that has been exposed to the recombinant enzyme or the recombinant protein.

The term "by use of recombinant DNA techniques" as used herein includes the anti-oxidant being any obtained by use of a recombinant enzyme or a recombinant protein, which enzyme or protein acts on the glucan. The term also includes the anti-oxidant being any obtained by use of an enzyme or protein, which enzyme or protein acts on a recombinant glucan.

The term "starch" in relation to the present invention includes native starch, degraded starch, modified starch, including its components amylose and amylopectin, and the glucose units thereof.

The terms "variant", "homologue" or "fragment" in relation to the enzyme include any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) amino acid from or to the sequence providing the resultant amino acid sequence has  $\alpha$ -glucan lyase activity, preferably having at least the same activity of any one of the enzymes shown as SEQ ID No. 1-6. In particular, the term "homologue" covers homology with respect to structure and/or function providing the resultant enzyme has  $\alpha$ -glucan lyase activity. With respect to sequence homology, preferably there is at least 75%, more preferably at least 85%, more preferably at least 90% homology to any one of the sequences shown as SEQ ID No.s 1-6. More

preferably there is at least 95%, more preferably at least 98%, homology to any one of the sequences shown as SEQ ID No. 1-6.

5 The terms "variant", "homologue" or "fragment" in relation to the nucleotide sequence coding for the enzyme include any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the sequence providing the resultant nucleotide sequence codes for an enzyme having  $\alpha$ -glucan lyase activity, preferably having at least the same activity of any one of the enzymes shown as SEQ ID No. 1-6. In particular, the term "homologue" covers  
10 homology with respect to structure and/or function providing the resultant nucleotide sequence codes for an enzyme having  $\alpha$ -glucan lyase activity. With respect to sequence homology, preferably there is at least 75%, more preferably at least 85%, more preferably at least 90% homology to any one of the sequences shown as SEQ ID No. 7-12. More preferably there is at least 95%, more preferably at least 98%,  
15 homology to any one of the sequences shown as SEQ ID No. 7-12.

The above terms are synonymous with allelic variations of the sequences.

20 The present invention also covers nucleotide sequences that can hybridise to the nucleotide sequence of the present invention.

The term "nucleotide" in relation to the present invention includes cDNA.

25 According to the present invention there is therefore provided a method of preparing *in situ* in an oxidisable medium an anti-oxidant. In a preferred embodiment, the anti-oxidant is anhydrofructose, more preferably 1,5-D-anhydrofructose. 1,5-D-anhydrofructose has been chemically synthesised (Lichtenthaler in Tetrahedron Letters Vol 21 pp 1429-1432). 1,5-D-anhydrofructose is further discussed in WO 95/10616, WO 95/10618 and GB-B-2294048.

30

The main advantages of using 1,5-D-anhydrofructose as an anti-oxidant are that it is a natural product, it is non-metabolisable, it is easy to manufacture, it is water-soluble, and it is generally non-toxic.

- 5 According to WO 95/10616, WO 95/10618 and GB-B-2294048, 1,5-D-anhydrofructose may be prepared by the enzymatic modification of substrates based on  $\alpha$ -1,4-glucan by use of the enzyme  $\alpha$ -1,4-glucan lyase. A typical  $\alpha$ -1,4-glucan based substrate is starch.
- 10 Today, starches have found wide uses in industry mainly because they are cheap raw materials. There are many references in the art to starch. For example, starch is discussed by Salisbury and Ross in Plant Physiology (Fourth Edition, 1991, Published by Wadsworth Publishing Company - especially section 11.7). In short, however, starch is one of the principal energy reserves of plants. It is often found in colourless
- 15 plastids (amyloplasts), in storage tissue and in the stroma of chloroplasts in many plants. Starch is a polysaccharide carbohydrate. It comprises two main components: amylose and/or amylopectin. Both amylose and/or amylopectin consist of straight chains of  $\alpha$ (1,4)-linked glucose units (ie glycosyl residues) but in addition amylopectin includes  $\alpha$ (1,6) branched glucose units.
- 20 Some of the glucan lyases discussed in WO 95/10616 and WO 95/10618 that are suitable for producing 1,5-D-anhydrofructose from starch are shown as SEQ I.D. No.s 1-4. Some of the glucan lyases discussed in GB-B-2294048 that are suitable for producing 1,5-D-anhydrofructose from starch are shown as SEQ I.D. No.s 5-6.
- 25 Some of the nucleotide sequences coding for glucan lyases discussed in WO 95/10616 and WO 95/10618 that are suitable for producing 1,5-D-anhydrofructose from starch are shown as SEQ I.D. No.s 7-10. Some of the nucleotide sequences coding for glucan lyases discussed in GB-B-2294048 that are suitable for producing 1,5-D-
- 30 anhydrofructose from starch are shown as SEQ I.D. No.s 11-12.

A further glucan lyase is discussed in WO 94/09122.

The recombinant nucleotide sequences coding for the enzyme may be cloned from sources such as a fungus, preferably *Morchella costata* or *Morchella vulgaris*, or from a fungally infected algae, preferably *Gracilariopsis lemaneiformis*, or from algae lone, preferably *Gracilariopsis lemaneiformis*.

5

In a preferred embodiment, the 1,5-D-anhydrofructose is prepared *in situ* by treating an  $\alpha$ -1,4-glucan with a recombinant  $\alpha$ -1,4-glucan lyase, such as any one of those presented as SEQ I.D. No.s 1-6.

10

Detailed commentary on how to prepare the enzymes shown as sequences SEQ I.D. No.s 1-6 may be found in the teachings of WO 95/10616, WO 95/10618 and GB-B-2294048. Likewise, detailed commentary on how to isolate and clone the nucleotide sequences SEQ I.D. No.s 7-12 may be found in the teachings of WO 95/10616, WO 95/10618 and GB-B-2294048.

15

If the glucan contains links other than and in addition to the  $\alpha$ -1,4- links the recombinant  $\alpha$ -1,4-glucan lyase can be used in conjunction with a suitable reagent that can break the other links - such as a recombinant hydrolase - preferably a recombinant glucanohydrolase.

20

General teachings of recombinant DNA techniques may be found in Sambrook, J., Fritsch, E.F., Maniatis T. (Editors) Molecular Cloning. A laboratory manual. Second edition. Cold Spring Harbour Laboratory Press. New York 1989.

25

In order to express a nucleotide sequence, the host organism can be a prokaryotic or a eukaryotic organism. Examples of suitable prokaryotic hosts include *E. coli* and *Bacillus subtilis*. Teachings on the transformation of prokaryotic hosts is well documented in the art, for example see Sambrook *et al* (Molecular Cloning: A Laboratory Manual, 2nd edition, 1989, Cold Spring Harbor Laboratory Press). If a

30

prokaryotic host is used then the gene may need to be suitably modified before transformation - such as by removal of introns.

In one embodiment, the host organism can be of the genus *Aspergillus*, such as *Aspergillus niger*. A transgenic *Aspergillus* can be prepared by following the teachings of Rambosek, J. and Leach, J. 1987 (Recombinant DNA in filamentous fungi: Progress and Prospects. CRC Crit. Rev. Biotechnol. 6:357-393), Davis R.W. 5 1994 (Heterologous gene expression and protein secretion in *Aspergillus*. In: Martinelli S.D., Kinghorn J.R.( Editors) *Aspergillus: 50 years on*. Progress in industrial microbiology vol 29. Elsevier Amsterdam 1994. pp 525-560), Ballance, D.J. 1991 (Transformation systems for Filamentous Fungi and an Overview of Fungal Gene structure. In: Leong, S.A., Berka R.M. (Editors) *Molecular Industrial* 10 *Mycology. Systems and Applications for Filamentous Fungi*. Marcel Dekker Inc. New York 1991. pp 1-29) and Turner G. 1994 (Vectors for genetic manipulation. In: Martinelli S.D., Kinghorn J.R.( Editors) *Aspergillus: 50 years on*. Progress in industrial microbiology vol 29. Elsevier Amsterdam 1994. pp. 641-666). However, the following commentary provides a summary of those teachings for producing 15 transgenic *Aspergillus*.

For almost a century, filamentous fungi have been widely used in many types of industry for the production of organic compounds and enzymes. For example, traditional Japanese koji and soy fermentations have used *Aspergillus sp.* Also, in this 20 century *Aspergillus niger* has been used for production of organic acids particular citric acid and for production of various enzymes for use in industry.

There are two major reasons why filamentous fungi have been so widely used in industry. First filamentous fungi can produce high amounts of extracellular products, 25 for example enzymes and organic compounds such as antibiotics or organic acids. Second filamentous fungi can grow on low cost substrates such as grains, bran, beet pulp etc. The same reasons have made filamentous fungi attractive organisms as hosts for heterologous expression of recombinant enzymes according to the present invention.

In order to prepare the transgenic *Aspergillus*, expression constructs are prepared by inserting a requisite nucleotide sequence into a construct designed for expression in filamentous fungi.

5 Several types of constructs used for heterologous expression have been developed. These constructs can contain a promoter which is active in fungi. Examples of promoters include a fungal promoter for a highly expressed extracellular enzyme, such as the glucoamylase promoter or the  $\alpha$ -amylase promoter. The nucleotide sequence can be fused to a signal sequence which directs the protein encoded by the nucleotide  
10 sequence to be secreted. Usually a signal sequence of fungal origin is used. A terminator active in fungi ends the expression system.

Another type of expression system has been developed in fungi where the nucleotide sequence can be fused to a smaller or a larger part of a fungal gene encoding a stable  
15 protein. This can stabilize the protein encoded by the nucleotide sequence. In such a system a cleavage site, recognized by a specific protease, can be introduced between the fungal protein and the protein encoded by the nucleotide sequence, so the produced fusion protein can be cleaved at this position by the specific protease thus liberating the protein encoded by the nucleotide sequence. By way of example, one  
20 can introduce a site which is recognized by a KEX-2 like peptidase found in at least some *Aspergilli*. Such a fusion leads to cleavage *in vivo* resulting in protection of the expressed product and not a larger fusion protein.

Heterologous expression in *Aspergillus* has been reported for several genes coding for  
25 bacterial, fungal, vertebrate and plant proteins. The proteins can be deposited intracellularly if the nucleotide sequence is not fused to a signal sequence. Such proteins will accumulate in the cytoplasm and will usually not be glycosylated which can be an advantage for some bacterial proteins. If the nucleotide sequence is equipped with a signal sequence the protein will accumulate extracellularly.

30

With regard to product stability and host strain modifications, some heterologous proteins are not very stable when they are secreted into the culture fluid of fungi.



Most fungi produce several extracellular proteases which degrade heterologous proteins. To avoid this problem special fungal strains with reduced protease production have been used as host for heterologous production.

5 For the transformation of filamentous fungi, several transformation protocols have been developed for many filamentous fungi (Ballance 1991, *ibid*). Many of them are based on preparation of protoplasts and introduction of DNA into the protoplasts using PEG and  $\text{Ca}^{2+}$  ions. The transformed protoplasts then regenerate and the transformed fungi are selected using various selective markers. Among the markers  
10 used for transformation are a number of auxotrophic markers such as *argB*, *trpC*, *niaD* and *pyrG*, antibiotic resistance markers such as benomyl resistance, hygromycin resistance and phleomycin resistance. A commonly used transformation marker is the *amdS* gene of *A. nidulans* which in high copy number allows the fungus to grow with acrylamide as the sole nitrogen source.

15

In another embodiment the transgenic organism can be a yeast. In this regard, yeast have also been widely used as a vehicle for heterologous gene expression. The species *Saccharomyces cerevisiae* has a long history of industrial use, including its use for heterologous gene expression. Expression of heterologous genes in  
20 *Saccharomyces cerevisiae* has been reviewed by Goodey *et al* (1987, Yeast Biotechnology, D R Berry *et al*, eds, pp 401-429, Allen and Unwin, London) and by King *et al* (1989, Molecular and Cell Biology of Yeasts, E F Walton and G T Yarronton, eds, pp 107-133, Blackie, Glasgow).

25 For several reasons *Saccharomyces cerevisiae* is well suited for heterologous gene expression. First, it is non-pathogenic to humans and it is incapable of producing certain endotoxins. Second, it has a long history of safe use following centuries of commercial exploitation for various purposes. This has led to wide public acceptability. Third, the extensive commercial use and research devoted to the  
30 organism has resulted in a wealth of knowledge about the genetics and physiology as well as large-scale fermentation characteristics of *Saccharomyces cerevisiae*.

A review of the principles of heterologous gene expression in *Saccharomyces cerevisiae* and secretion of gene products is given by E Hinchcliffe E Kenny (1993, "Yeast as a vehicle for the expression of heterologous genes", Yeasts, Vol 5, Anthony H Rose and J Stuart Harrison, eds, 2nd edition, Academic Press Ltd.).

5

Several types of yeast vectors are available, including integrative vectors, which require recombination with the host genome for their maintenance, and autonomously replicating plasmid vectors.

10 In order to prepare the transgenic *Saccharomyces*, expression constructs are prepared by inserting the nucleotide sequence into a construct designed for expression in yeast. Several types of constructs used for heterologous expression have been developed. The constructs contain a promoter active in yeast fused to the nucleotide sequence, usually a promoter of yeast origin, such as the GAL1 promoter, is used. Usually a  
15 signal sequence of yeast origin, such as the sequence encoding the SUC2 signal peptide, is used. A terminator active in yeast ends the expression system.

For the transformation of yeast several transformation protocols have been developed. For example, a transgenic *Saccharomyces* can be prepared by following the teachings  
20 of Hinnen *et al* (1978, Proceedings of the National Academy of Sciences of the USA 75, 1929); Beggs, J D (1978, Nature, London, 275, 104); and Ito, H *et al* (1983, J Bacteriology 153, 163-168).

The transformed yeast cells are selected using various selective markers. Among the  
25 markers used for transformation are a number of auxotrophic markers such as LEU2, HIS4 and TRP1, and dominant antibiotic resistance markers such as aminoglycoside antibiotic markers, eg G418.

Another host organism is a plant. In this regard, the art is replete with references for  
30 preparing transgenic plants. Two documents that provide some background commentary on the types of techniques that may be employed to prepare transgenic plants are EP-B-0470145 and CA-A-2006454 - some of which commentary is

presented below.

The basic principle in the construction of genetically modified plants is to insert genetic information in the plant genome so as to obtain a stable maintenance of the  
5 inserted genetic material.

Several techniques exist for inserting the genetic information, the two main principles being direct introduction of the genetic information and introduction of the genetic information by use of a vector system. A review of the general techniques may be  
10 found in articles by Potrykus (Annu Rev Plant Physiol Plant Mol Biol [1991] 42:205-225) and Christou (Agro-Food-Industry Hi-Tech March/April 1994 17-27).

Thus, in one aspect, the present invention relates to a vector system which carries a recombinant nucleotide sequence and which is capable of introducing the nucleotide  
15 sequence into the genome of an organism, such as a plant, and wherein the nucleotide sequence is capable of preparing *in situ* an anti-oxidant.

The vector system may comprise one vector, but it can comprise at least two vectors. In the case of two vectors, the vector system is normally referred to as a binary  
20 vector system. Binary vector systems are described in further detail in Gynheung An et al. (1980), Binary Vectors, *Plant Molecular Biology Manual A3*, 1-19.

One extensively employed system for transformation of plant cells with a given promoter or nucleotide sequence or construct is based on the use of a Ti plasmid from  
25 *Agrobacterium tumefaciens* or a Ri plasmid from *Agrobacterium rhizogenes* (An et al. (1986), *Plant Physiol.* 81, 301-305 and Butcher D.N. et al. (1980), *Tissue Culture Methods for Plant Pathologists*, eds.: D.S. Ingrams and J.P. Helgeson, 203-208).

Several different Ti and Ri plasmids have been constructed which are suitable for the  
30 construction of the plant or plant cell constructs described above.

The nucleotide sequence of the present invention should preferably be inserted into

the Ti-plasmid between the border sequences of the T-DNA or adjacent a T-DNA sequence so as to avoid disruption of the sequences immediately surrounding the T-DNA borders, as at least one of these regions appear to be essential for insertion of modified T-DNA into the plant genome.

5

As will be understood from the above explanation, if the organism is a plant, then the vector system of the present invention is preferably one which contains the sequences necessary to infect the plant (e.g. the *vir* region) and at least one border part of a T-DNA sequence, the border part being located on the same vector as the genetic  
10 construct. Preferably, the vector system is an *Agrobacterium tumefaciens* Ti-plasmid or an *Agrobacterium rhizogenes* Ri-plasmid or a derivative thereof, as these plasmids are well-known and widely employed in the construction of transgenic plants, many vector systems exist which are based on these plasmids or derivatives thereof.

15

In the construction of a transgenic plant the nucleotide sequence or construct or vector of the present invention may be first constructed in a microorganism in which the vector can replicate and which is easy to manipulate before insertion into the plant. An example of a useful microorganism is *E. coli.*, but other microorganisms having the above properties may be used. When a vector of a vector system as defined  
20 above has been constructed in *E. coli.* it is transferred, if necessary, into a suitable *Agrobacterium* strain, e.g. *Agrobacterium tumefaciens*. The Ti-plasmid harbouring the first nucleotide sequence or construct of the invention is thus preferably transferred into a suitable *Agrobacterium* strain, e.g. *A. tumefaciens*, so as to obtain an *Agrobacterium* cell harbouring the promoter or nucleotide sequence or construct  
25 of the invention, which DNA is subsequently transferred into the plant cell to be modified.

30

As reported in CA-A-2006454, a large number of cloning vectors are available which contain a replication system in *E. coli* and a marker which allows a selection of the transformed cells. The vectors contain for example pBR322, the pUC series, the M13 mp series, pACYC 184 etc. In this way, the promoter or nucleotide or construct of the present invention can be introduced into a suitable restriction position

in the vector. The contained plasmid is used for the transformation in *E. coli*. The *E. coli* cells are cultivated in a suitable nutrient medium and then harvested and lysed. The plasmid is then recovered and then analysed - such as by any one or more of the following techniques: sequence analysis, restriction analysis, electrophoresis and  
5 further biochemical-molecular biological methods. After each manipulation, the used DNA sequence can be restricted or selectively amplified by PCR techniques and connected with the next DNA sequence. Each sequence can be cloned in the same or different plasmid.

10 After each introduction method of the nucleotide sequence or construct or vector according to the present invention in the plants the presence and/or insertion of further DNA sequences may be necessary. If, for example, for the transformation the Ti- or Ri-plasmid of the plant cells is used, at least the right boundary and often however the right and the left boundary of the Ti- and Ri-plasmid T-DNA, as  
15 flanking areas of the introduced genes, can be connected. The use of T-DNA for the transformation of plant cells has been intensively studied and is described in EP-A-120516; Hoekema, in: The Binary Plant Vector System Offset-drukkerij Kanters B.B., Alblaserdam, 1985, Chapter V; Fraley, *et al.*, Crit. Rev. Plant Sci., 4:1-46; and An *et al.*, EMBO J. (1985) 4:277-284.

20 Direct infection of plant tissues by *Agrobacterium* is a simple technique which has been widely employed and which is described in Butcher D.N. *et al.* (1980), *Tissue Culture Methods for Plant Pathologists*, eds.: D.S. Ingrams and J.P. Helgeson, 203-208. For further teachings on this topic see Potrykus (Annu Rev Plant Physiol Plant  
25 Mol Biol [1991] 42:205-225) and Christou (Agro-Food-Industry Hi-Tech March/April 1994 17-27). With this technique, infection of a plant may be done on a certain part or tissue of the plant, i.e. on a part of a leaf, a root, a stem or another part of the plant.

30 Typically, with direct infection of plant tissues by *Agrobacterium* carrying the first nucleotide sequence or the construct, a plant to be infected is wounded, e.g. by cutting the plant with a razor or puncturing the plant with a needle or rubbing the

plant with an abrasive. The wound is then inoculated with the *Agrobacterium*. The inoculated plant or plant part is then grown on a suitable culture medium.

5 When plant cells are constructed, these cells are grown and, optionally, maintained in a medium according to the present invention following well-known tissue culturing methods - such as by culturing the cells in a suitable culture medium supplied with the necessary growth factors such as amino acids, plant hormones, vitamins, etc, but wherein the culture medium comprises a component according to the present invention. Regeneration of the transformed cells into genetically modified plants may  
10 be accomplished using known methods for the regeneration of plants from cell or tissue cultures, for example by selecting the transformed shoots and by subculturing the shoots on a medium containing the appropriate nutrients, plant hormones, etc.

Further teachings on plant transformation may be found in EP-A-0449375.  
15

Reference may even be made to Spngstad *et al* (1995 Plant Cell Tissue Organ Culture 40 pp 1-15) as these authors present a general overview on transgenic plant construction.

20 In one embodiment, the plant is a grapevine. There are a number of teachings in the art on how to prepare transformed grapevines. For example, reference may be made to Baribault *et al* (J Exp Bot 41 (229) 1990 1045-1050), Baribault *et al* (Plant Cell Rep 8 (3) 1989 137-140), Scorza *et al* (J Am Soc Horticultural Science 121 (4) 1996 616-619), Kikkert *et al* (Plant Cell Reports 15 (5) 1996 311-316), Golles *et al* (Acta  
25 Hortic 1997 vol 447 Number: Horticultural Biotechnology in Vitro Culture and Breeding Pages 265-275), Gray and Scorza (WO-A-97/49277) and Simon Robinson *et al* (Conference abstracts and paper presented in Biotechnology - Food and Health for the 21st Century, Adelaide, Australia, 1998). By way of example Robinson *et al* (*ibid*) disclose a method for transforming grapevine wherein somatic embryos are  
30 induced on callus formed from another tissue and *Agrobacterium* infection is used to transfer target genes into the embryo tissue.

Further reference may be made to the teachings of Andrew Walker in Nature Biotechnology (Vol 14, May 1996, page 582) who states that:

5           *"The grape, one of the most important fruit plants in the world, has been difficult to engineer because of its high levels of tannins and phenols, which interfere with cell culture and transformation; the compounds oxidize quickly and promote the decay of grape cells."*

10           In that same edition of Nature Biotechnology, Perl *et al* (pages 624-628) report on the use of the combination of polyvinylpyrrolidone and dithiothreitol to improve the viability of grape transformation during *Agrobacterium* infection.

15           Hence, the present invention provides an alternative means for transforming grape. In this regard, the antioxidant that is prepared *in situ* by a grape transformed in accordance with the present invention improves the viability of grape transformation during *Agrobacterium* infection.

20           Thus, according to one aspect of the present invention, there is provided the use of an antioxidant prepared *in situ* in order to effectively transform a grape.

25           In some instances, it is desirable for the recombinant enzyme or protein to be easily secreted into the medium to act as or to generate an anti-oxidant therein. In such cases, the DNA encoding the recombinant enzyme is fused to *inter alia* an appropriate signal sequence, an appropriate promoter and an appropriate terminator from the chosen host.

30           For example, for expression in *Aspergillus niger* the *gpdA* (from the Glyceraldehyde-3-phosphate dehydrogenase gene of *Aspergillus nidulans*) promoter and signal sequence is fused to the 5' end of the DNA encoding the mature lyase. The terminator sequence from the *A. niger trpC* gene is placed 3' to the gene (Punt, P.J. et al 1991 - (1991): J. Biotech. 17, 19-34). This construction is inserted into a vector containing a replication origin and selection origin for *E. coli* and a selection marker

for *A. niger*. -Examples of selection markers for *A. niger* are the amdS gene, the argB gene, the pyrG gene, the hygB gene, the BmlR gene which all have been used for selection of transformants. This plasmid can be transformed into *A. niger* and the mature lyase can be recovered from the culture medium of the transformants.

5 Eventually the construction could be transformed into a protease deficient strain to reduce the proteolytic degradation of the lyase in the medium (Archer D.B. et al 1992 -Biotechnol. Lett. 14, 357-362).

In addition, and as indicated above, aside from using *Aspergillus niger* as the host,

10 there are other industrial important microorganisms which could be used as expression systems. Examples of these other hosts include: *Aspergillus oryzae*, *Aspergillus sp.*, *Trichoderma sp.*, *Saccharomyces cerevisiae*, *Kluyveromyces sp.*, *Hansenula sp.*, *Pichia sp.*, *Bacillus subtilis*, *B. amyloliquefaciens*, *Bacillus sp.*, *Streptomyces sp.* or *E. coli*.

15 In accordance with the present invention, a suitable marker or selection means may be introduced into the host that is to be transformed with the nucleotide sequence. Examples of suitable markers or selection means are described in any one of WO-A-93/05163, WO-A-94/20627, GB patent application No. 9702591.0 (filed 7 February

20 1997), GB patent application No. 9702576.1 (filed 7 February 1997), GB patent application No. 9702539.9 (filed 7 February 1997), GB patent application No. 9702510.0 (filed 7 February 1997) and GB patent application No. 9702592.8 (filed 7 February 1997).

25 In summation, the present invention relates to a process comprising preparing a medium that comprises an anti-oxidant and at least one other component, the process comprising preparing *in situ* in the medium the anti-oxidant; and wherein the anti-oxidant is prepared from a glucan by use of recombinant DNA techniques and/or the anti-oxidant is prepared by use of a recombinant glucan lyase.

30



In a preferred embodiment, the present invention relates to a process a process of preparing a medium that comprises an anti-oxidant and at least one other component, the process comprising preparing *in situ* in the medium the anti-oxidant; and wherein the anti-oxidant is prepared from a glucan by use of a recombinant glucan lyase.

5

In a more preferred embodiment, the present invention relates to a process of preparing a medium that comprises an anti-oxidant and at least one other component, the process comprising preparing *in situ* in the medium the anti-oxidant; wherein the anti-oxidant is prepared from a glucan by use of a recombinant glucan lyase; and

10 wherein the anti-oxidant is anhydro-fructose.

The present invention will now be described only by way of example.

#### TRANSGENIC GRAPE

15

Transformed grapes are prepared following the teachings of Perl *et al (ibid)* but wherein the use of the combination of polyvinylpyrrolidone and dithiothreitol is optional. In these studies, the grapes are transformed with any one of the nucleotide sequences presented as SEQ ID No. 7-12. The transformation leads to *in situ*

20 preparation of 1,5-D-anhydrofructose. The transformed grapes are beneficial for one or more of the reasons mentioned earlier.

Details on these studies are as follows.

#### 25 Tissue-culture systems for transformation studies

The long term somatic embryogenic callus culture is developed from the vegetative tissues of anthers of *Vitis vinifera* CV Superior Seedless. Methods for another culture, induction of somatic embryogenesis and maintenance of embryogenic

30 cultures, are previously described (Perl *et al*, 1995, Plant Sci 104: 193-200). Briefly, embryogenic calli are maintained on solidified (0.25% gelrite) MS medium (Murashige and Skoog, 1962, Physiol Plant 15: 473-497) supplemented with 6%

sucrose, 2 mg/L 2,4-dichlorophenoxyacetic acid (2,4-D), 5 mg/L Indole-3-aspartic acid (IASP), 0.2 mg/L 6-benzyladenine (BAP) and 1 mg/L abscisic acid (ABA). Proembryogenic calli are induced by transferring the calli to MS medium supplemented with the same phytohormones, but 2,4-D is substituted with 2 mg/L 2-naphthoxyacetic acid (NOA). This stage is used for transformation experiments.

### *Agrobacterium* strains

For studying the sensitivity of grape embryogenic calli to the presence of different *Agrobacterium* strains, or for stable transformation experiments, cocultivation is attempted using the following *A. tumefaciens* strains: EHA 101-p492 (Perl *et al.*, 1993, Bio/Technology 11:715-718); LBA 4404-pGPTV (Becker *et al.*, 1992, Plant Mol Biol 20: 1195-1197); and GVE 3101-pPCV91 (Vancanneyt *et al.*, 1990, Mol Gen Genet 220: 245-250). These strains contain the binary vectors conferring resistance to kanamycin (*nptII*), basta (*bar*) and hygromycin (*hpt*), respectively, all under the control of the nopaline-synthase (NOS) promoter and terminator. Bacteria are cultured with the proper antibiotics in liquid LB medium for 24 hours at 28°C at 200 rpm.

### Cocultivation

For studying the sensitivity of grape embryogenic calli to different *Agrobacterium* strains, bacterial cultures with different optical densities (0.1-0.7 at 630 nm) are prepared from an overnight culture of *Agrobacterium* strains. Bacteria are centrifuged 5 minutes, 5000 rpm and resuspended in antibiotic free McCown's Woody Plant Medium (WPM) (Lloyd and McCown, 1981, Int Plant Prop Soc Proc 30: 421-427). Three grams fresh weight of embryogenic calli (7 days after transfer to NOA containing medium) are resuspended in 10 ml of overnight cultured bacterial suspensions for 5 minutes, dry blotted and transferred to Petri dishes containing regeneration medium [basal WPM medium supplemented with thidiazuron (TDZ) (0.5 mg/L), Zeatin riboside (ZR) (0.5 mg/L), and sucrose (3%)]. The regeneration medium is solidified with gelrite (0.25% w/v) and the calli, after initial drainage of excess bacteria, are cocultivated in the dark at 25°C for different times (5 minutes

up to 7 days). For stable transformation experiments, inoculum (OD 0.6 at 630 nm) is prepared from an overnight culture of LBA 4404 or GVE 3101. Bacteria are centrifuged 5 minutes, 5000 rpm and resuspended in antibiotic-free WPM medium. Embryogenic calli (3g fresh weight) are resuspended in 10 ml of bacteria for 5 minutes, dry blotted and transferred to Petri dishes containing solidified (0.25% w/v) gelrite regeneration medium supplemented with different antioxidants. The calli are cocultivated for 48 hours in the dark at 25°C.

### Selective culture

Following 48 hours of cocultivation, the embryogenic callus is maintained in the dark for 7 days on antioxidant containing regeneration medium. Subsequently, the calli are collected on a sterile metal screen and transferred to fresh WPM regeneration medium at 25°C under 40  $\mu\text{E}/\text{m}^2/\text{s}$  (white fluorescent tubes). All regeneration media are supplemented with 400 mg/L claforan, 1.5 g/L malt extract and different selectable markers: kanamycin (50-500 mg/L), hygromycin (15 mg/L) and Basta (1-10 mg/L). Periodic increases in hygromycin concentration are used. The putative transformed calli are cultured on regeneration medium supplemented with 15 mg/L hygromycin. Every two weeks the regenerating calli are transferred to fresh medium supplemented with 20 and 25 mg/L hygromycin respectively. Control, untransformed grape calli are also cultured on selective media and are periodically exposed to increasing hygromycin concentrations. Green adventitious embryos, which developed on calli cultured for 8-10 weeks on selective regeneration medium, are transferred to germination medium. Embryo germination, rooting and subsequent plantlet development are induced on WPM as described (Perl *et al*, 1995, Plant Sci **104**: 193-200), supplemented with 25 mg/L hygromycin or 10 mg/L basta. Conversion of vitrified abnormal plantlets into normal-looking grape plantlets are obtained using solidified WPM medium supplemented with 0.1 mg/L NAA as described (Perl *et al*, 1995, Plant Sci **104**: 193-200).

## TRANSGENIC POTATOES

General teachings on potato transformation may be found in our copending patent applications PCT/EP96/03053, PCT/EP96/03052 and PCT/EP94/01082 (the contents  
5 of each of which are incorporated herein by reference).

For the present studies, the following protocol is adopted.

### Plasmid construction

10

The disarmed *Agrobacterium tumefaciens* strain LBA 4404, containing the helper *vir* plasmid pRAL4404 (Hoekema *et al*, 1983 Nature 303 pp 179-180), is cultured on YMB agar (K<sub>2</sub>HPO<sub>4</sub>·3H<sub>2</sub>O 660 mg l<sup>-1</sup>, MgSO<sub>4</sub> 200 mg l<sup>-1</sup>, NaCl 100 mg l<sup>-1</sup>, mannitol 10 g l<sup>-1</sup>, yeast extract 400 mg l<sup>-1</sup>, 0.8% w/v agar, pH 7.0) containing 100 mg l<sup>-1</sup>  
15 rifampicin and 500 mg l<sup>-1</sup> streptomycin sulphate. Transformation with pVICTOR IV GNG E35S *nagB* IV2' or pVICTOR IV GNG *rbc nagB* IV2' or pVICTOR IV GNG E35S *nagB*' (which correspond to each of pVICTOR IV GNG E35S *nagB* IV2 or pVICTOR IV GNG *rbc nagB* IV2 or pVICTOR IV GNG E35S *nagB* but wherein each of those plasmids also contains any one of the nucleotide sequences shown as  
20 SEQ ID No.s. 7-12 operatively linked to a functional promoter) is accomplished using the freeze-thaw method of Holters *et al* (1978 Mol Gen Genet 163 181-187) and transformants are selected on YMB agar containing 100 mg l<sup>-1</sup> rifampicin and 500 mg l<sup>-1</sup> streptomycin, and 50 mg l<sup>-1</sup> gentamycin sulphate.

### 25 Transformation of plants

Shoot cultures of *Solanum tuberosum* cv Saturna are maintained on LS agar containing Murashige Skoog basal salts (Sigma M6899) (Murashige and Skoog, 1965, Physiol Plant 15 473-497) with 2 μM silver thiosulphate, and nutrients and vitamins  
30 as described by Linsmaier and Skoog (1965 Physiol Plant 18 100-127). Cultures are maintained at 25°C with a 16h daily photoperiod. After approximately 40 days, subculturing is performed during which leaves are removed, and the shoots cut into

mononodal segments of approximately 8 mm length.

Shoot cultures of approximately 40 days maturity (5-6 cm height) are cut into 8 mm internodal segments which are placed into liquid LS-medium containing  
5 *Agrobacterium tumefaciens* transformed with pVICTOR IV GNG E35S *nagB* IV2' or pVICTOR IV GNG *rbc nagB* IV2' or pVICTOR IV GNG E35S *nagB*' ( $A_{660} = 0.5$ , pathlength 1 cm). Following incubation at room temperature for 30 minutes, the segments are dried by blotting on to sterile filter paper and transferred to LS agar (0.8% w/v containing 2 mg l<sup>-1</sup> 2,4-D and 500 µg l<sup>-1</sup> trans-zeatin. The explants are  
10 covered with filter paper, moistened with LS medium, and covered with a cloth for three days at 25°C. Following this treatment, the segments are washed with liquid LS medium containing 800 mg l<sup>-1</sup> carbenicillin, and transferred on to LS agar (0.8% w/v) containing 1 mg l<sup>-1</sup> trans-zeatin, 100 µg l<sup>-1</sup> gibberellic acid (GA3), with sucrose (eg 7.5 g l<sup>-1</sup>) and glucosamine (eg 2.5 g l<sup>-1</sup>) as the selection agent.

15

The segments are sub-cultured to fresh substrate each 3-4 weeks. In 3 to 4 weeks, shoots develop from the segments and the formation of new shoots continues for 3-4 months.

#### 20 Rooting of regenerated shoots

The regenerated shoots are transferred to rooting substrate composed of LS-substrate, agar (8 g/l) and carbenicillin (800 mg/l).

25 The transgenic plants may be verified by performing a GUS assay on the co-introduced β-glucuronidase gene according to Hodal, L. *et al.* (Pl. Sci. (1992), 87: 115-122).

Alternatively, the transgenic genotype of the regenerated shoot may be verified by  
30 performing NPTII assays (Radke, S. E. *et al.*, Theor. Appl. Genet. (1988), 75: 685-694) or by performing PCR analysis according to Wang *et al.* (1993, NAR 21 pp 4153-4154).

### Transfer to soil

The newly rooted plants (height approx. 2-3 cms) are transplanted from rooting substrate to soil and placed in a growth chamber (21°C, 16 hour light 200-  
5 400uE/m<sup>2</sup>/sec). When the plants are well established they are transferred to the greenhouse, where they are grown until tubers had developed and the upper part of the plants are senescing.

### Harvesting

10

The potatoes are harvested after about 3 months.

## TRANSGENIC MAIZE PLANTS

### 15 **Introduction**

Since the first publication of production of transgenic plants in 1983 (Leemans, 1993  
Biotechnology 11 s22), there have been numerous publications of production of  
transgenic plants including especially dicotyledon crop plants.

20

Until very recently there are very few reports on successful production of transgenic  
monocotyledonary crop plants. This relatively slow development within monocots  
are due to two causes. Firstly, until the early 1980s, efficient regeneration of plants  
from cultured cells and tissues of monocots had proven very difficult. This problem  
25 is ultimately solved by the culture of explants from immature and embryogenic tissue,  
which retain their morphogenic potential on nutrient media containing plant growth  
regulators. Secondly, the monocots are not a natural host for *Agrobacterium  
tumefaciens*, meaning that the successful developed techniques within the dicots using  
their natural vector *Agrobacterium tumefaciens* is unsuccessful for many years in the  
30 monocots.

Nevertheless, it is now possible to successfully transformation and produce fertile

transgenic plants of maize using methods such as: (1) Silicon Carbide Whiskers; (2) Particle Bombardment; (3) DNA Uptake by PEG treated protoplast; or (4) DNA Uptake in Electroporation of Tissue. Each of these methods - which are reviewed by Thompson (1995 *Euphytica* 85 pp 75-80) - may be used to prepare *inter alia* transgenic maize according to the present invention.

In particular, the particle Gun method has been successfully used for the transformation of monocots. However, EP-A-0604662 reports on a different method of transforming monocotyledons. The method comprises transforming cultured tissues of a monocotyledon under or after dedifferentiation with *Agrobacterium* containing a super binary vector as a selectable marker a hygromycin-resistant gene is used. Production of transgenic calli and plant is demonstrated using the hygromycin selection. This method may be used to prepare *inter alia* transgenic maize according to the present invention.

Subsequent to the method of EP-A-0604662, EP-A-0672752 reports on non-dedifferentiated immature embryos. In this regard, both hygromycin-resistance and PPT-resistance genes are used as the selectable marker, with PPT giving rise to 10% or more independent transformed plants. This method may be used to prepare *inter alia* transgenic maize according to the present invention.

To date, it would appear that transgenic maize plants can be successfully produced from easily-culturable varieties - such as the inbred line A188. In this regard, see the teachings of Ishida *et al* (1996 *Nature Biotechnology* 14 pp 745-750). The method disclosed by these workers may be used to prepare *inter alia* transgenic maize according to the present invention.

Vasil (1996 *Nature Biotechnology* 14 pp 702-703) presents a further review article on transformation of maize. Even though it is possible to prepare transformed maize by use of, for example, particle Gun mediated transformation, for the present studies the following protocol is adopted.

### Plasmid construction

The disarmed *Agrobacterium tumefaciens* strain LBA 4404, containing the helper *vir* plasmid pRAL4404 (Hoekema *et al.*, 1983 Nature 303 pp 179-180), is cultured on  
5 YMB agar ( $K_2HPO_4 \cdot 3H_2O$  660 mg l<sup>-1</sup>,  $MgSO_4$  200 mg l<sup>-1</sup>, NaCl 100 mg l<sup>-1</sup>, mannitol 10 g l<sup>-1</sup>, yeast extract 400 mg l<sup>-1</sup>, 0.8% w/v agar, pH 7.0) containing 100 mg l<sup>-1</sup> rifampicin and 500 mg l<sup>-1</sup> streptomycin sulphate. Transformation with pVICTOR IV GNG E35S *nagB* IV2' or pVICTOR IV GNG *rbc nagB* IV2' or pVICTOR IV GNG E35S *nagB*' is accomplished using the freeze-thaw method of Holters *et al.* (1978 Mol  
10 Gen Genet 163 181-187) and transformants are selected on YMB agar containing 100 mg l<sup>-1</sup> rifampicin and 500 mg l<sup>-1</sup> streptomycin, and 50 mg l<sup>-1</sup> gentamycin sulphate.

### Isolation and cocultivation of explants

15 Immature embryos of, for example, maize line A188 of the size between 1.5 to 2.5 mm are isolated and cocultivated with *Agrobacterium tumefaciens* strain LBA 4404 in N6-AS for 2-3 days at 25°C under illumination. Thereafter, the embryos are washed with sterilized water containing 250 mg/l of cefotaxime and transferred to an LS medium and 250 mg/l cefotaxime and glucosamine in concentrations of up to 100  
20 mg/l (the medium is hereafter called LSS1).

### Conditions for the selection of transgenic plants

The explants are cultured for three weeks on LSS1 medium and then transferred to  
25 an LS medium containing glucosamine and cefotaxime. After three weeks on this medium, green shoots are isolated.

### Rooting of transformed shoots

30 Transformed shoots are transferred to an MS medium containing 2 mg/l for rooting. After four weeks on this medium, plantlets are transferred to pots with sterile soil for acclimatisation.



**TRANSGENIC GUAR PLANTS**

Transformation of guar cotyledonary explants is performed according to Joersbo and Okkels (PCT/DK95/00221) using *Agrobacterium tumefaciens* LBA4404 harbouring  
5 a suitable plasmid.

Other plants may be transformed in accordance with the present invention, such as other fruits, other vegetables, and other plants such as coffee plants, tea plants etc.

10 Other modifications of the present invention will be apparent to those skilled in the art.

## SEQUENCES

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: DANISCO A/S  
 (B) STREET: LANGEBROGADE 1  
 (C) CITY: COPENHAGEN  
 (D) STATE: COPENHAGEN K  
 (E) COUNTRY: DENMARK  
 (F) POSTAL CODE (ZIP): DK-1001

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1088 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Phe Ser Thr Leu Ala Phe Val Ala Pro Ser Ala Leu Gly Ala Ser  
 1 5 10 15  
 Thr Phe Val Gly Ala Glu Val Arg Ser Asn Val Arg Ile His Ser Ala  
 20 25 30  
 Phe Pro Ala Val His Thr Ala Thr Arg Lys Thr Asn Arg Leu Asn Val  
 35 40 45  
 Ser Met Thr Ala Leu Ser Asp Lys Gln Thr Ala Thr Ala Gly Ser Thr  
 50 55 60  
 Asp Asn Pro Asp Gly Ile Asp Tyr Lys Thr Tyr Asp Tyr Val Gly Val  
 65 70 75 80  
 Trp Gly Phe Ser Pro Leu Ser Asn Thr Asn Trp Phe Ala Ala Gly Ser  
 85 90 95  
 Ser Thr Pro Gly Gly Ile Thr Asp Trp Thr Ala Thr Met Asn Val Asn  
 100 105 110  
 Phe Asp Arg Ile Asp Asn Pro Ser Ile Thr Val Gln His Pro Val Gln  
 115 120 125  
 Val Gln Val Thr Ser Tyr Asn Asn Asn Ser Tyr Arg Val Arg Phe Asn  
 130 135 140  
 Pro Asp Gly Pro Ile Arg Asp Val Thr Arg Gly Pro Ile Leu Lys Gln  
 145 150 155 160  
 Gln Leu Asp Trp Ile Arg Thr Gln Glu Leu Ser Glu Gly Cys Asp Pro  
 165 170 175  
 Gly Met Thr Phe Thr Ser Glu Gly Phe Leu Thr Phe Glu Thr Lys Asp  
 180 185 190  
 Leu Ser Val Ile Ile Tyr Gly Asn Phe Lys Thr Arg Val Thr Arg Lys  
 195 200 205  
 Ser Asp Gly Lys Val Ile Met Glu Asn Asp Glu Val Gly Thr Ala Ser  
 210 215 220  
 Ser Gly Asn Lys Cys Arg Gly Leu Met Phe Val Asp Arg Leu Tyr Gly  
 225 230 235 240  
 Asn Ala Ile Ala Ser Val Asn Lys Asn Phe Arg Asn Asp Ala Val Lys  
 245 250 255  
 Gln Glu Gly Phe Tyr Gly Ala Gly Glu Val Asn Cys Lys Tyr Gln Asp  
 260 265 270  
 Thr Tyr Ile Leu Glu Arg Thr Gly Ile Ala Met Thr Asn Tyr Asn Tyr  
 275 280 285  
 Asp Asn Leu Asn Tyr Asn Gln Trp Asp Leu Arg Pro Pro His His Asp  
 290 295 300  
 Gly Ala Leu Asn Pro Asp Tyr Tyr Ile Pro Met Tyr Tyr Ala Ala Pro  
 305 310 315 320  
 Trp Leu Ile Val Asn Gly Cys Ala Gly Thr Ser Glu Gln Tyr Ser Tyr  
 325 330 335  
 Gly Trp Phe Met Asp Asn Val Ser Gln Ser Tyr Met Asn Thr Gly Asp  
 340 345 350

Thr Thr Trp Asn Ser Gly Gln Glu Asp Leu Ala Tyr Met Gly Ala Gln  
 355 360 365  
 Tyr Gly Pro Phe Asp Gln His Phe Val Tyr Gly Ala Gly Gly Gly Met  
 370 375 380  
 Glu Cys Val Val Thr Ala Phe Ser Leu Leu Gln Gly Lys Glu Phe Glu  
 385 390 400  
 Asn Gln Val Leu Asn Lys Arg Ser Val Met Pro Pro Lys Tyr Val Phe  
 405 410 415  
 Gly Phe Phe Gln Gly Val Phe Gly Thr Ser Ser Leu Leu Arg Ala His  
 420 425 430  
 Met Pro Ala Gly Glu Asn Asn Ile Ser Val Glu Glu Ile Val Glu Gly  
 435 440 445  
 Tyr Gln Asn Asn Asn Phe Pro Phe Glu Gly Leu Ala Val Asp Val Asp  
 450 455 460  
 Met Gln Asp Asn Leu Arg Val Phe Thr Thr Lys Gly Glu Phe Trp Thr  
 465 470 475 480  
 Ala Asn Arg Val Gly Thr Gly Gly Asp Pro Asn Asn Arg Ser Val Phe  
 485 490 495  
 Glu Trp Ala His Asp Lys Gly Leu Val Cys Gln Thr Asn Ile Thr Cys  
 500 505 510  
 Phe Leu Arg Asn Asp Asn Glu Gly Gln Asp Tyr Glu Val Asn Gln Thr  
 515 520 525  
 Leu Arg Glu Arg Gln Leu Tyr Thr Lys Asn Asp Ser Leu Thr Gly Thr  
 530 535 540  
 Asp Phe Gly Met Thr Asp Asp Gly Pro Ser Asp Ala Tyr Ile Gly His  
 545 550 555 560  
 Leu Asp Tyr Gly Gly Val Glu Cys Asp Ala Leu Phe Pro Asp Trp  
 565 570 575  
 Gly Arg Pro Asp Val Ala Glu Trp Trp Gly Asn Asn Tyr Lys Lys Leu  
 580 585 590  
 Phe Ser Ile Gly Leu Asp Phe Val Trp Gln Asp Met Thr Val Pro Ala  
 595 600 605  
 Met Met Pro His Lys Ile Gly Asp Asp Ile Asn Val Lys Pro Asp Gly  
 610 615 620  
 Asn Trp Pro Asn Ala Asp Asp Pro Ser Asn Gly Gln Tyr Asn Trp Lys  
 625 630 635 640  
 Thr Tyr His Pro Gln Val Leu Val Thr Asp Met Arg Tyr Glu Asn His  
 645 650 655  
 Gly Arg Glu Pro Met Val Thr Gln Arg Asn Ile His Ala Tyr Thr Leu  
 660 665 670  
 Cys Glu Ser Thr Arg Lys Glu Gly Ile Val Glu Asn Ala Asp Thr Leu  
 675 680 685  
 Thr Lys Phe Arg Arg Ser Tyr Ile Ile Ser Arg Gly Gly Tyr Ile Gly  
 690 695 700  
 Asn Gln His Phe Gly Gly Met Trp Val Gly Asp Asn Ser Thr Thr Ser  
 705 710 715 720  
 Asn Tyr Ile Gln Met Met Ile Ala Asn Asn Ile Asn Met Asn Met Ser  
 725 730 735  
 Cys Leu Pro Leu Val Gly Ser Asp Ile Gly Gly Phe Thr Ser Tyr Asp  
 740 745 750  
 Asn Glu Asn Gln Arg Thr Pro Cys Thr Gly Asp Leu Met Val Arg Tyr  
 755 760 765  
 Val Gln Ala Gly Cys Leu Leu Pro Trp Phe Arg Asn His Tyr Asp Arg  
 770 775 780  
 Trp Ile Glu Ser Lys Asp His Gly Lys Asp Tyr Gln Glu Leu Tyr Met  
 785 790 795 800  
 Tyr Pro Asn Glu Met Asp Thr Leu Arg Lys Phe Val Glu Phe Arg Tyr  
 805 810 815  
 Arg Trp Gln Glu Val Leu Tyr Thr Ala Met Tyr Gln Asn Ala Ala Phe  
 820 825 830  
 Gly Lys Pro Ile Ile Lys Ala Ala Ser Met Tyr Asn Asn Asp Ser Asn  
 835 840 845  
 Val Arg Arg Ala Gln Asn Asp His Phe Leu Leu Gly Gly His Asp Gly  
 850 855 860  
 Tyr Arg Ile Leu Cys Ala Pro Val Val Trp Glu Asn Ser Thr Glu Arg  
 865 870 875 880

Glu Leu Tyr Leu Pro Val Leu Thr Gln Trp Tyr Lys Phe Gly Pro Asp  
 885 890 895  
 Phe Asp Thr Lys Pro Leu Glu Gly Ala Met Asn Gly Gly Asp Arg Ile  
 900 905 910  
 Tyr Asn Tyr Pro Val Pro Gln Ser Glu Ser Pro Ile Phe Val Arg Glu  
 915 920 925  
 Gly Ala Ile Leu Pro Thr Arg Tyr Thr Leu Asn Gly Glu Asn Lys Ser  
 930 935 940  
 Leu Asn Thr Tyr Thr Asp Glu Asp Pro Leu Val Phe Glu Val Phe Pro  
 945 950 955 960  
 Leu Gly Asn Asn Arg Ala Asp Gly Met Cys Tyr Leu Asp Asp Gly Gly  
 965 970 975  
 Val Thr Thr Asn Ala Glu Asp Asn Gly Lys Phe Ser Val Val Lys Val  
 980 985 990  
 Ala Ala Glu Gln Asp Gly Gly Thr Glu Thr Ile Thr Phe Thr Asn Asp  
 995 1000 1005  
 Cys Tyr Glu Tyr Val Phe Gly Gly Pro Phe Tyr Val Arg Val Arg Gly  
 1010 1015 1020  
 Ala Gln Ser Pro Ser Asn Ile His Val Ser Ser Gly Ala Gly Ser Gln  
 1025 1030 1035 1040  
 Asp Met Lys Val Ser Ser Ala Thr Ser Arg Ala Ala Leu Phe Asn Asp  
 1045 1050 1055  
 Gly Glu Asn Gly Asp Phe Trp Val Asp Gln Glu Thr Asp Ser Leu Trp  
 1060 1065 1070  
 Leu Lys Leu Pro Asn Val Val Leu Pro Asp Ala Val Ile Thr Ile Thr  
 1075 1080 1085

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1091 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Tyr Pro Thr Leu Thr Phe Val Ala Pro Ser Ala Leu Gly Ala Arg  
 1 5 10 15  
 Thr Phe Thr Cys Val Gly Ile Phe Arg Ser His Ile Leu Ile His Ser  
 20 25 30  
 Val Val Pro Ala Val Arg Leu Ala Val Arg Lys Ser Asn Arg Leu Asn  
 35 40 45  
 Val Ser Met Ser Ala Leu Phe Asp Lys Pro Thr Ala Val Thr Gly Gly  
 50 55 60  
 Lys Asp Asn Pro Asp Asn Ile Asn Tyr Thr Thr Tyr Asp Tyr Val Pro  
 65 70 75 80  
 Val Trp Arg Phe Asp Pro Leu Ser Asn Thr Asn Trp Phe Ala Ala Gly  
 85 90 95  
 Ser Ser Thr Pro Gly Asp Ile Asp Asp Trp Thr Ala Thr Met Asn Val  
 100 105 110  
 Asn Phe Asp Arg Ile Asp Asn Pro Ser Phe Thr Leu Glu Lys Pro Val  
 115 120 125  
 Gln Val Gln Val Thr Ser Tyr Lys Asn Asn Cys Phe Arg Val Arg Phe  
 130 135 140  
 Asn Pro Asp Gly Pro Ile Arg Asp Val Asp Arg Gly Pro Ile Leu Gln  
 145 150 155 160  
 Gln Gln Leu Asn Trp Ile Arg Lys Gln Glu Gln Ser Lys Gly Phe Asp  
 165 170 175  
 Pro Lys Met Gly Phe Thr Lys Glu Gly Phe Leu Lys Phe Glu Thr Lys  
 180 185 190  
 Asp Leu Asn Val Ile Ile Tyr Gly Asn Phe Lys Thr Arg Val Thr Arg  
 195 200 205  
 Lys Arg Asp Gly Lys Gly Ile Met Glu Asn Asn Glu Val Pro Ala Gly  
 210 215 220

Ser Leu Gly Asn Lys Cys Arg Gly Leu Met Phe Val Asp Arg Leu Tyr  
 225 230 235 240  
 Gly Thr Ala Ile Ala Ser Val Asn Glu Asn Tyr Arg Asn Asp Pro Asp  
 245 250 255  
 Arg Lys Glu Gly Phe Tyr Gly Ala Gly Glu Val Asn Cys Glu Phe Trp  
 260 265 270  
 Asp Ser Glu Gln Asn Arg Asn Lys Tyr Ile Leu Glu Arg Thr Gly Ile  
 275 280 285  
 Ala Met Thr Asn Tyr Asn Tyr Asp Asn Tyr Asn Tyr Asn Gln Ser Asp  
 290 295 300  
 Leu Ile Ala Pro Gly Tyr Pro Ser Asp Pro Asn Phe Tyr Ile Pro Met  
 305 310 315 320  
 Tyr Phe Ala Ala Pro Trp Val Val Val Lys Gly Cys Ser Gly Asn Ser  
 325 330 335  
 Asp Glu Gln Tyr Ser Tyr Gly Trp Phe Met Asp Asn Val Ser Gln Thr  
 340 345 350  
 Tyr Met Asn Thr Gly Gly Thr Ser Trp Asn Cys Gly Glu Glu Asn Leu  
 355 360 365  
 Ala Tyr Met Gly Ala Gln Cys Gly Pro Phe Asp Gln His Phe Val Tyr  
 370 375 380  
 Gly Asp Gly Asp Gly Leu Glu Asp Val Val Gln Ala Phe Ser Leu Leu  
 385 390 395 400  
 Gln Gly Lys Glu Phe Glu Asn Gln Val Leu Asn Lys Arg Ala Val Met  
 405 410 415  
 Pro Pro Lys Tyr Val Phe Gly Tyr Phe Gln Gly Val Phe Gly Ile Ala  
 420 425 430  
 Ser Leu Leu Arg Glu Gln Arg Pro Glu Gly Gly Asn Asn Ile Ser Val  
 435 440 445  
 Gln Glu Ile Val Glu Gly Tyr Gln Ser Asn Asn Phe Pro Leu Glu Gly  
 450 455 460  
 Leu Ala Val Asp Val Asp Met Gln Gln Asp Leu Arg Val Phe Thr Thr  
 465 470 475 480  
 Lys Ile Glu Phe Trp Thr Ala Asn Lys Val Gly Thr Gly Gly Asp Ser  
 485 490 495  
 Asn Asn Lys Ser Val Phe Glu Trp Ala His Asp Lys Gly Leu Val Cys  
 500 505 510  
 Gln Thr Asn Val Thr Cys Phe Leu Arg Asn Asp Asn Gly Gly Ala Asp  
 515 520 525  
 Tyr Glu Val Asn Gln Thr Leu Arg Glu Lys Gly Leu Tyr Thr Lys Asn  
 530 535 540  
 Asp Ser Leu Thr Asn Thr Asn Phe Gly Thr Thr Asn Asp Gly Pro Ser  
 545 550 555 560  
 Asp Ala Tyr Ile Gly His Leu Asp Tyr Gly Gly Gly Gly Asn Cys Asp  
 565 570 575  
 Ala Leu Phe Pro Asp Trp Gly Arg Pro Gly Val Ala Glu Trp Trp Gly  
 580 585 590  
 Asp Asn Tyr Ser Lys Leu Phe Lys Ile Gly Leu Asp Phe Val Trp Gln  
 595 600 605  
 Asp Met Thr Val Pro Ala Met Met Pro His Lys Val Gly Asp Ala Val  
 610 615 620  
 Asp Thr Arg Ser Pro Tyr Gly Trp Pro Asn Glu Asn Asp Pro Ser Asn  
 625 630 635 640  
 Gly Arg Tyr Asn Trp Lys Ser Tyr His Pro Gln Val Leu Val Thr Asp  
 645 650 655  
 Met Arg Tyr Glu Asn His Gly Arg Glu Pro Met Phe Thr Gln Arg Asn  
 660 665 670  
 Met His Ala Tyr Thr Leu Cys Glu Ser Thr Arg Lys Glu Gly Ile Val  
 675 680 685  
 Ala Asn Ala Asp Thr Leu Thr Lys Phe Arg Arg Ser Tyr Ile Ile Ser  
 690 695 700  
 Arg Gly Gly Tyr Ile Gly Asn Gln His Phe Gly Gly Met Trp Val Gly  
 705 710 715 720  
 Asp Asn Ser Ser Ser Gln Arg Tyr Leu Gln Met Met Ile Ala Asn Ile  
 725 730 735  
 Val Asn Met Asn Met Ser Cys Leu Pro Leu Val Gly Ser Asp Ile Gly  
 740 745 750

Gly Phe Thr-Ser Tyr Asp Gly Arg Asn Val Cys Pro Gly Asp Leu Met  
 755 760 765  
 Val Arg Phe Val Gln Ala Gly Cys Leu Leu Pro Trp Phe Arg Asn His  
 770 775 780  
 Tyr Gly Arg Leu Val Glu Gly Lys Gln Glu Gly Lys Tyr Tyr Gln Glu  
 785 790 795 800  
 Leu Tyr Met Tyr Lys Asp Glu Met Ala Thr Leu Arg Lys Phe Ile Glu  
 805 810 815  
 Phe Arg Tyr Arg Trp Gln Glu Val Leu Tyr Thr Ala Met Tyr Gln Asn  
 820 825 830  
 Ala Ala Phe Gly Lys Pro Ile Ile Lys Ala Ala Ser Met Tyr Asp Asn  
 835 840 845  
 Asp Arg Asn Val Arg Gly Ala Gln Asp Asp His Phe Leu Leu Gly Gly  
 850 855 860  
 His Asp Gly Tyr Arg Ile Leu Cys Ala Pro Val Val Trp Glu Asn Thr  
 865 870 875 880  
 Thr Ser Arg Asp Leu Tyr Leu Pro Val Leu Thr Lys Trp Tyr Lys Phe  
 885 890 895  
 Gly Pro Asp Tyr Asp Thr Lys Arg Leu Asp Ser Ala Leu Asp Gly Gly  
 900 905 910  
 Gln Met Ile Lys Asn Tyr Ser Val Pro Gln Ser Asp Ser Pro Ile Phe  
 915 920 925  
 Val Arg Glu Gly Ala Ile Leu Pro Thr Arg Tyr Thr Leu Asp Gly Ser  
 930 935 940  
 Asn Lys Ser Met Asn Thr Tyr Thr Asp Lys Asp Pro Leu Val Phe Glu  
 945 950 955 960  
 Val Phe Pro Leu Gly Asn Asn Arg Ala Asp Gly Met Cys Tyr Leu Asp  
 965 970 975  
 Asp Gly Gly Ile Thr Thr Asp Ala Glu Asp His Gly Lys Phe Ser Val  
 980 985 990  
 Ile Asn Val Glu Ala Leu Arg Lys Gly Val Thr Thr Thr Ile Lys Phe  
 995 1000 1005  
 Ala Tyr Asp Thr Tyr Gln Tyr Val Phe Asp Gly Pro Phe Tyr Val Arg  
 1010 1015 1020  
 Ile Arg Asn Leu Thr Thr Ala Ser Lys Ile Asn Val Ser Ser Gly Ala  
 1025 1030 1035 1040  
 Gly Glu Glu Asp Met Thr Pro Thr Ser Ala Asn Ser Arg Ala Ala Leu  
 1045 1050 1055  
 Phe Ser Asp Gly Gly Val Gly Glu Tyr Trp Ala Asp Asn Asp Thr Ser  
 1060 1065 1070  
 Ser Leu Trp Met Lys Leu Pro Asn Leu Val Leu Gln Asp Ala Val Ile  
 1075 1080 1085  
 Thr Ile Thr  
 1090

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1066 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ala Gly Phe Ser Asp Pro Leu Asn Phe Cys Lys Ala Glu Asp Tyr  
 1 5 10 15  
 Tyr Ser Val Ala Leu Asp Trp Lys Gly Pro Gln Lys Ile Ile Gly Val  
 20 25 30  
 Asp Thr Thr Pro Pro Lys Ser Thr Lys Phe Pro Lys Asn Trp His Gly  
 35 40 45  
 Val Asn Leu Arg Phe Asp Asp Gly Thr Leu Gly Val Val Gln Phe Ile  
 50 55 60  
 Arg Pro Cys Val Trp Arg Val Arg Tyr Asp Pro Gly Phe Lys Thr Ser  
 65 70 75 80

Asp Glu Tyr-Gly Asp Glu Asn Thr Arg Thr Ile Val Gln Asp Tyr Met  
 85 90 95  
 Ser Thr Leu Ser Asn Lys Leu Asp Thr Tyr Arg Gly Leu Thr Trp Glu  
 100 105 110  
 Thr Lys Cys Glu Asp Ser Gly Asp Phe Phe Thr Phe Ser Ser Lys Val  
 115 120 125  
 Thr Ala Val Glu Lys Ser Glu Arg Thr Arg Asn Lys Val Gly Asp Gly  
 130 135 140  
 Leu Arg Ile His Leu Trp Lys Ser Pro Phe Arg Ile Gln Val Val Arg  
 145 150 155 160  
 Thr Leu Thr Pro Leu Lys Asp Pro Tyr Pro Ile Pro Asn Val Ala Ala  
 165 170 175  
 Ala Glu Ala Arg Val Ser Asp Lys Val Val Trp Gln Thr Ser Pro Lys  
 180 185 190  
 Thr Phe Arg Lys Asn Leu His Pro Gln His Lys Met Leu Lys Asp Thr  
 195 200 205  
 Val Leu Asp Ile Val Lys Pro Gly His Gly Glu Tyr Val Gly Trp Gly  
 210 215 220  
 Glu Met Gly Gly Ile Gln Phe Met Lys Glu Pro Thr Phe Met Asn Tyr  
 225 230 235 240  
 Phe Asn Phe Asp Asn Met Gln Tyr Gln Gln Val Tyr Ala Gln Gly Ala  
 245 250 255  
 Leu Asp Ser Arg Glu Pro Leu Tyr His Ser Asp Pro Phe Tyr Leu Asp  
 260 265 270  
 Val Asn Ser Asn Pro Glu His Lys Asn Ile Thr Ala Thr Phe Ile Asp  
 275 280 285  
 Asn Tyr Ser Gln Ile Ala Ile Asp Phe Gly Lys Thr Asn Ser Gly Tyr  
 290 295 300  
 Ile Lys Leu Gly Thr Arg Tyr Gly Gly Ile Asp Cys Tyr Gly Ile Ser  
 305 310 315 320  
 Ala Asp Thr Val Pro Glu Ile Val Arg Leu Tyr Thr Gly Leu Val Gly  
 325 330 335  
 Arg Ser Lys Leu Lys Pro Arg Tyr Ile Leu Gly Ala His Gln Ala Cys  
 340 345 350  
 Tyr Gly Tyr Gln Gln Glu Ser Asp Leu Tyr Ser Val Val Gln Gln Tyr  
 355 360 365  
 Arg Asp Cys Lys Phe Pro Leu Asp Gly Ile His Val Asp Val Asp Val  
 370 375 380  
 Gln Asp Gly Phe Arg Thr Phe Thr Thr Asn Pro His Thr Phe Pro Asn  
 385 390 395 400  
 Pro Lys Glu Met Phe Thr Asn Leu Arg Asn Asn Gly Ile Lys Cys Ser  
 405 410 415  
 Thr Asn Ile Thr Pro Val Ile Ser Ile Asn Asn Arg Glu Gly Gly Tyr  
 420 425 430  
 Ser Thr Leu Leu Glu Gly Val Asp Lys Lys Tyr Phe Ile Met Asp Asp  
 435 440 445  
 Arg Tyr Thr Glu Gly Thr Ser Gly Asn Ala Lys Asp Val Arg Tyr Met  
 450 455 460  
 Tyr Tyr Gly Gly Gly Asn Lys Val Glu Val Asp Pro Asn Asp Val Asn  
 465 470 475 480  
 Gly Arg Pro Asp Phe Lys Asp Asn Tyr Asp Phe Pro Ala Asn Phe Asn  
 485 490 495  
 Ser Lys Gln Tyr Pro Tyr His Gly Gly Val Ser Tyr Gly Tyr Gly Asn  
 500 505 510  
 Gly Ser Ala Gly Phe Tyr Pro Asp Leu Asn Arg Lys Glu Val Arg Ile  
 515 520 525  
 Trp Trp Gly Met Gln Tyr Lys Tyr Leu Phe Asp Met Gly Leu Glu Phe  
 530 535 540  
 Val Trp Gln Asp Met Thr Pro Ala Ile His Thr Ser Tyr Gly Asp  
 545 550 555 560  
 Met Lys Gly Leu Pro Thr Arg Leu Leu Val Thr Ser Asp Ser Val Thr  
 565 570 575  
 Asn Ala Ser Glu Lys Lys Leu Ala Ile Glu Thr Trp Ala Leu Tyr Ser  
 580 585 590  
 Tyr Asn Leu His Lys Ala Thr Trp His Gly Leu Ser Arg Leu Glu Ser  
 595 600 605

Arg Lys Asn Lys Arg Asn Phe Ile Leu Gly Arg Gly Ser Tyr Ala Gly  
 610 615 620  
 Ala Tyr Arg Phe Ala Gly Leu Trp Thr Gly Asp Asn Ala Ser Asn Trp  
 625 630 635 640  
 Glu Phe Trp Lys Ile Ser Val Ser Gln Val Leu Ser Leu Gly Leu Asn  
 645 650 655  
 Gly Val Cys Ile Ala Gly Ser Asp Thr Gly Gly Phe Glu Pro Tyr Arg  
 660 665 670  
 Asp Ala Asn Gly Val Glu Glu Lys Tyr Cys Ser Pro Glu Leu Ile  
 675 680 685  
 Arg Trp Tyr Thr Gly Ser Phe Leu Leu Pro Trp Leu Arg Asn His Tyr  
 690 695 700  
 Val Lys Lys Asp Arg Lys Trp Phe Gln Glu Pro Tyr Ser Tyr Pro Lys  
 705 710 715 720  
 His Leu Glu Thr His Pro Glu Leu Ala Asp Gln Ala Trp Leu Tyr Lys  
 725 730 735  
 Ser Val Leu Glu Ile Cys Arg Tyr Tyr Val Glu Leu Arg Tyr Ser Leu  
 740 745 750  
 Ile Gln Leu Leu Tyr Asp Cys Met Phe Gln Asn Val Val Asp Gly Met  
 755 760 765  
 Pro Ile Thr Arg Ser Met Leu Leu Thr Asp Thr Glu Asp Thr Thr Phe  
 770 775 780  
 Phe Asn Glu Ser Gln Lys Phe Leu Asp Asn Gln Tyr Met Ala Gly Asp  
 785 790 795 800  
 Asp Ile Leu Val Ala Pro Ile Leu His Ser Arg Lys Glu Ile Pro Gly  
 805 810 815  
 Glu Asn Arg Asp Val Tyr Leu Pro Leu Tyr His Thr Trp Tyr Pro Ser  
 820 825 830  
 Asn Leu Arg Pro Trp Asp Asp Gln Gly Val Ala Leu Gly Asn Pro Val  
 835 840 845  
 Glu Gly Gly Ser Val Ile Asn Tyr Thr Ala Arg Ile Val Ala Pro Glu  
 850 855 860  
 Asp Tyr Asn Leu Phe His Ser Val Val Pro Val Tyr Val Arg Glu Gly  
 865 870 875 880  
 Ala Ile Ile Pro Gln Ile Glu Val Arg Gln Trp Thr Gly Gln Gly Gly  
 885 890 895  
 Ala Asn Arg Ile Lys Phe Asn Ile Tyr Pro Gly Lys Asp Lys Glu Tyr  
 900 905 910  
 Cys Thr Tyr Leu Asp Asp Gly Val Ser Arg Asp Ser Ala Pro Glu Asp  
 915 920 925  
 Leu Pro Gln Tyr Lys Glu Thr His Glu Gln Ser Lys Val Glu Gly Ala  
 930 935 940  
 Glu Ile Ala Lys Gln Ile Gly Lys Lys Thr Gly Tyr Asn Ile Ser Gly  
 945 950 955 960  
 Thr Asp Pro Glu Ala Lys Gly Tyr His Arg Lys Val Ala Val Thr Gln  
 965 970 975  
 Thr Ser Lys Asp Lys Thr Arg Thr Val Thr Ile Glu Pro Lys His Asn  
 980 985 990  
 Gly Tyr Asp Pro Ser Lys Glu Val Gly Asp Tyr Tyr Thr Ile Ile Leu  
 995 1000 1005  
 Trp Tyr Ala Pro Gly Phe Asp Gly Ser Ile Val Asp Val Ser Lys Thr  
 1010 1015 1020  
 Thr Val Asn Val Glu Gly Gly Val Glu His Gln Val Tyr Lys Asn Ser  
 1025 1030 1035 1040  
 Asp Leu His Thr Val Val Ile Asp Val Lys Glu Val Ile Gly Thr Thr  
 1045 1050 1055  
 Lys Ser Val Lys Ile Thr Cys Thr Ala Ala  
 1060 1065



## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Gly Leu Ser Asp Pro Leu Asn Phe Cys Lys Ala Glu Asp Tyr  
 1 5 10 15  
 Tyr Ala Ala Ala Lys Gly Trp Ser Gly Pro Gln Lys Ile Ile Arg Tyr  
 20 25 30  
 Asp Gln Thr Pro Pro Gln Gly Thr Lys Asp Pro Lys Ser Trp His Ala  
 35 40 45  
 Val Asn Leu Pro Phe Asp Asp Gly Thr Met Cys Val Val Gln Phe Val  
 50 55 60  
 Arg Pro Cys Val Trp Arg Val Arg Tyr Asp Pro Ser Val Lys Thr Ser  
 65 70 75 80  
 Asp Glu Tyr Gly Asp Glu Asn Thr Arg Thr Ile Val Gln Asp Tyr Met  
 85 90 95  
 Thr Thr Leu Val Gly Asn Leu Asp Ile Phe Arg Gly Leu Thr Trp Val  
 100 105 110  
 Ser Thr Leu Glu Asp Ser Gly Glu Tyr Tyr Thr Phe Lys Ser Glu Val  
 115 120 125  
 Thr Ala Val Asp Glu Thr Glu Arg Thr Arg Asn Lys Val Gly Asp Gly  
 130 135 140  
 Leu Lys Ile Tyr Leu Trp Lys Asn Pro Phe Arg Ile Gln Val Val Arg  
 145 150 155 160  
 Leu Leu Thr Pro Leu Val Asp Pro Phe Pro Ile Pro Asn Val Ala Asn  
 165 170 175  
 Ala Thr Ala Arg Val Ala Asp Lys Val Val Trp Gln Thr Ser Pro Lys  
 180 185 190  
 Thr Phe Arg Lys Asn Leu His Pro Gln His Lys Met Leu Lys Asp Thr  
 195 200 205  
 Val Leu Asp Ile Ile Lys Pro Gly His Gly Glu Tyr Val Gly Trp Gly  
 210 215 220  
 Glu Met Gly Gly Ile Glu Phe Met Lys Glu Pro Thr Phe Met Asn Tyr  
 225 230 235 240  
 Phe Asn Phe Asp Asn Met Gln Tyr Gln Gln Val Tyr Ala Gln Gly Ala  
 245 250 255  
 Leu Asp Ser Arg Glu Pro Leu Tyr His Ser Asp Pro Phe Tyr Leu Asp  
 260 265 270  
 Val Asn Ser Asn Pro Glu His Lys Asn Ile Thr Ala Thr Phe Ile Asp  
 275 280 285  
 Asn Tyr Ser Gln Ile Ala Ile Asp Phe Gly Lys Thr Asn Ser Gly Tyr  
 290 295 300  
 Ile Lys Leu Gly Thr Arg Tyr Gly Gly Ile Asp Cys Tyr Gly Ile Ser  
 305 310 315 320  
 Ala Asp Thr Val Pro Glu Ile Val Arg Leu Tyr Thr Gly Leu Val Gly  
 325 330 335  
 Arg Ser Lys Leu Lys Pro Arg Tyr Ile Leu Gly Ala His Gln Ala Cys  
 340 345 350  
 Tyr Gly Tyr Gln Gln Glu Ser Asp Leu His Ala Val Val Gln Gln Tyr  
 355 360 365  
 Arg Asp Thr Lys Phe Pro Leu Asp Gly Leu His Val Asp Val Asp Phe  
 370 375 380  
 Gln Asp Asn Phe Arg Thr Phe Thr Thr Asn Pro Ile Thr Phe Pro Asn  
 385 390 395 400  
 Pro Lys Glu Met Phe Thr Asn Leu Arg Asn Asn Gly Ile Lys Cys Ser  
 405 410 415  
 Thr Asn Ile Thr Pro Val Ile Ser Ile Arg Asp Arg Pro Asn Gly Tyr  
 420 425 430  
 Ser Thr Leu Asn Glu Gly Tyr Asp Lys Lys Tyr Phe Ile Met Asp Asp  
 435 440 445

Arg Tyr Thr Glu Gly Thr Ser Gly Asp Pro Gln Asn Val Arg Tyr Ser  
 450 455 460  
 Phe Tyr Gly Gly Gly Asn Pro Val Glu Val Asn Pro Asn Asp Val Trp  
 465 470 475  
 Ala Arg Pro Asp Phe Gly Asp Asn Tyr Asp Phe Pro Thr Asn Phe Asn  
 485 490 495  
 Cys Lys Asp Tyr Pro Tyr His Gly Gly Val Ser Tyr Gly Tyr Gly Asn  
 500 505 510  
 Gly Thr Pro Gly Tyr Tyr Pro Asp Leu Asn Arg Glu Glu Val Arg Ile  
 515 520 525  
 Trp Trp Gly Leu Gln Tyr Glu Tyr Leu Phe Asn Met Gly Leu Glu Phe  
 530 535 540  
 Val Trp Gln Asp Met Thr Pro Ala Ile His Ser Ser Tyr Gly Asp  
 545 550 555 560  
 Met Lys Gly Leu Pro Thr Arg Leu Leu Val Thr Ala Asp Ser Val Thr  
 565 570 575  
 Asn Ala Ser Glu Lys Lys Leu Ala Ile Glu Ser Trp Ala Leu Tyr Ser  
 580 585 590  
 Tyr Asn Leu His Lys Ala Thr Phe His Gly Leu Gly Arg Leu Glu Ser  
 595 600 605  
 Arg Lys Asn Lys Arg Asn Phe Ile Leu Gly Arg Gly Ser Tyr Ala Gly  
 610 615 620  
 Ala Tyr Arg Phe Ala Gly Leu Trp Thr Gly Asp Asn Ala Ser Thr Trp  
 625 630 635 640  
 Glu Phe Trp Lys Ile Ser Val Ser Gln Val Leu Ser Leu Gly Leu Asn  
 645 650 655  
 Gly Val Cys Ile Ala Gly Ser Asp Thr Gly Gly Phe Glu Pro Ala Arg  
 660 665 670  
 Thr Glu Ile Gly Glu Glu Lys Tyr Cys Ser Pro Glu Leu Leu Ile Arg  
 675 680 685  
 Trp Tyr Thr Gly Ser Phe Leu Leu Pro Trp Leu Arg Asn His Tyr Val  
 690 695 700  
 Lys Lys Asp Arg Lys Trp Phe Gln Glu Pro Tyr Ala Tyr Pro Lys His  
 705 710 715 720  
 Leu Glu Thr His Pro Glu Leu Ala Asp Gln Ala Trp Leu Tyr Lys Ser  
 725 730 735  
 Val Leu Glu Ile Cys Arg Tyr Trp Val Glu Leu Arg Tyr Ser Leu Ile  
 740 745 750  
 Gln Leu Leu Tyr Asp Cys Met Phe Gln Asn Val Val Asp Gly Met Pro  
 755 760 765  
 Leu Ala Arg Ser Met Leu Leu Thr Asp Thr Glu Asp Thr Thr Phe Phe  
 770 775 780  
 Asn Glu Ser Gln Lys Phe Leu Asp Asn Gln Tyr Met Ala Gly Asp Asp  
 785 790 795 800  
 Ile Leu Val Ala Pro Ile Leu His Ser Arg Asn Glu Val Pro Gly Glu  
 805 810 815  
 Asn Arg Asp Val Tyr Leu Pro Leu Phe His Thr Trp Tyr Pro Ser Asn  
 820 825 830  
 Leu Arg Pro Trp Asp Asp Gln Gly Val Ala Leu Gly Asn Pro Val Glu  
 835 840 845  
 Gly Gly Ser Val Ile Asn Tyr Thr Ala Arg Ile Val Ala Pro Glu Asp  
 850 855 860  
 Tyr Asn Leu Phe His Asn Val Val Pro Val Tyr Ile Arg Glu Gly Ala  
 865 870 875 880  
 Ile Ile Pro Gln Ile Gln Val Arg Gln Trp Ile Gly Glu Gly Gly Pro  
 885 890 895  
 Asn Pro Ile Lys Phe Asn Ile Tyr Pro Gly Lys Asp Lys Glu Tyr Val  
 900 905 910  
 Thr Tyr Leu Asp Asp Gly Val Ser Arg Asp Ser Ala Pro Asp Asp Leu  
 915 920 925  
 Pro Gln Tyr Arg Glu Ala Tyr Glu Gln Ala Lys Val Glu Gly Lys Asp  
 930 935 940  
 Val Gln Lys Gln Leu Ala Val Ile Gln Gly Asn Lys Thr Asn Asp Phe  
 945 950 955 960  
 Ser Ala Ser Gly Ile Asp Lys Glu Ala Lys Gly Tyr His Arg Lys Val  
 965 970 975

Ser Ile Lys-Gln Glu Ser Lys Asp Lys Thr Arg Thr Val Thr Ile Glu  
 980 985 990  
 Pro Lys His Asn Gly Tyr Asp Pro Ser Lys Glu Val Gly Asn Tyr Tyr  
 995 1000 1005  
 Thr Ile Ile Leu Trp Tyr Ala Pro Gly Phe Asp Gly Ser Ile Val Asp  
 1010 1015 1020  
 Val Ser Gln Ala Thr Val Asn Ile Glu Gly Gly Val Glu Cys Glu Ile  
 1025 1030 1035 1040  
 Phe Lys Asn Thr Gly Leu His Thr Val Val Val Asn Val Lys Glu Val  
 1045 1050 1055  
 Ile Gly Thr Thr Lys Ser Val Lys Ile Thr Cys Thr Thr Ala  
 1060 1065 1070

SEQ. ID. NO. 5

SEQUENCE TYPE: ENZYME  
 MOLECULE TYPE: AMINO ACID  
 ORIGINAL SOURCE: ALGAL  
 SEQUENCE LENGTH: 1092 AMINO ACIDS  
 SEQUENCE:

	5	10	15
1	Met	Phe	Pro
16	Ser	Thr	Phe
31	Ser	Ala	Leu
46	Tyr	Asn	Val
61	Ser	Ile	Gly
76	Asp	Tyr	Ile
91	Trp	Tyr	Ala
106	Thr	Ala	Thr
121	Tyr	Ser	Asn
136	Asn	Asn	Ser
151	Asp	Val	Ser
166	Arg	Ser	Gln
181	Ser	Pro	Glu
196	Ile	Ile	Tyr
211	Tyr	Leu	Val
226	Asn	Lys	Cys
241	Ala	Ile	Ala
256	Asn	Glu	Lys
271	Glu	Gln	Gly
286	Ala	Met	Thr
301	Asp	Val	Val
316	Pro	Met	Tyr
331	Gly	Thr	Ser
346	Ser	Gln	Ser
361	Gln	Glu	Asn
376	Gln	His	Phe
391	Lys	Ala	Phe
406	Leu	Asn	Lys
421	Phe	Gln	Gly
436	Pro	Ala	Gly
451	Tyr	Gln	Asp
466	Asp	Met	Gln
481	Trp	Ser	Ala
496	Ser	Val	Phe
511	Asn	Val	Thr
526	Glu	Val	Asn
541	Asp	Ser	Leu
556	Gly	Asp	Ala
571	Cys	Asp	Ala
586	Trp	Trp	Gly
601	Phe	Val	Trp
616	Leu	Gly	Asp
631	Trp	Pro	Asn
646	Ser	Tyr	His
661	Glu	Tyr	Gly

676 Tyr Thr Leu Cys Glu Ser Thr Arg-Arg Glu Gly Ile Val Gly Asn  
 691 Ala Asp Ser Leu Thr Lys Phe Arg Arg Ser Tyr Ile Ile Ser Arg  
 706 Gly Gly Tyr Ile Gly Asn Gln His Phe Gly Gly Met Trp Val Gly  
 721 Asp Asn Ser Ala Thr Glu Ser Tyr Leu Gln Met Met Leu Ala Asn  
 736 Ile Ile Asn Met Asn Met Ser Cys Leu Pro Leu Val Gly Ser Asp  
 751 Ile Gly Gly Phe Thr Gln Tyr Asn Asp Ala Gly Asp Pro Thr Pro  
 766 Glu Asp Leu Met Val Arg Phe Val Gln Ala Gly Cys Leu Leu Pro  
 781 Trp Phe Arg Asn His Tyr Asp Arg Trp Ile Glu Ser Lys Lys His  
 796 Gly Lys Lys Tyr Gln Glu Leu Tyr Met Tyr Pro Gly Gln Lys Asp  
 811 Thr Leu Lys Lys Phe Val Glu Phe Arg Tyr Arg Trp Gln Glu Val  
 826 Leu Tyr Thr Ala Met Tyr Gln Asn Ala Thr Thr Gly Glu Pro Ile  
 841 Ile Lys Ala Ala Pro Met Tyr Asn Asn Asp Val Asn Val Tyr Lys  
 856 Ser Gln Asn Asp His Phe Leu Leu Gly Gly His Asp Gly Tyr Arg  
 871 Ile Leu Cys Ala Pro Val Arg Glu Asn Ala Thr Ser Arg Glu  
 886 Val Tyr Leu Pro Val Tyr Ser Lys Trp Phe Lys Phe Gly Pro Asp  
 901 Phe Asp Thr Lys Pro Leu Glu Asn Glu Ile Gln Gly Gly Gln Thr  
 916 Leu Tyr Asn Tyr Ala Ala Pro Leu Asn Asp Ser Pro Ile Phe Val  
 931 Arg Glu Gly Thr Ile Leu Pro Thr Arg Tyr Thr Leu Asp Gly Val  
 946 Asn Lys Ser Ile Asn Thr Tyr Thr Asp Asn Asp Pro Leu Val Phe  
 961 Glu Leu Phe Pro Leu Glu Asn Asn Gln Ala His Gly Leu Phe Tyr  
 976 His Asp Asp Gly Gly Val Thr Thr Asn Ala Glu Asp Phe Gly Lys  
 991 Tyr Ser Val Ile Ser Val Lys Ala Ala Gln Gly Ser Gln Met  
 1006 Ser Val Lys Phe Asp Asn Glu Val Tyr Glu His Gln Trp Gly Ala  
 1021 Ser Phe Tyr Val Arg Val Arg Asn Met Gly Ala Pro Ser Asn Ile  
 1036 Asn Val Ser Ser Gln Ile Gly Gln Gln Asp Met Gln Gln Ser Ser  
 1051 Val Ser Ser Arg Ala Gln Met Phe Thr Ser Ala Asn Asp Gly Glu  
 1066 Tyr Trp Val Asp Gln Ser Thr Asn Ser Leu Trp Leu Lys Leu Pro  
 1081 Gly Ala Val Ile Gln Asp Ala Ala Ile Thr Val Arg

Number of amino acid residues: 1092

Amino acid composition (including the signal sequence):

64 Ala	14 Cys	18 His	33 Met	56 Thr
48 Arg	55 Gln	45 Ile	49 Phe	22 Trp
89 Asn	49 Glu	65 Leu	59 Pro	67 Tyr
73 Asp	94 Gly	46 Lys	73 Ser	73 Val

SEQ. ID. NO. 6

SEQUENCE TYPE: ENZYME  
 MOLECULE TYPE: AMINO ACID  
 ORIGINAL SOURCE: ALGAL  
 SEQUENCE LENGTH: 570 AMINO ACIDS  
 SEQUENCE:

				5						10					15
1	Met	Thr	Asn	Tyr	Asn	Tyr	Asp	Asn	Leu	Asn	Tyr	Asn	Gln	Pro	Asp
16	Leu	Ile	Pro	Pro	Gly	His	Asp	Ser	Asp	Pro	Asp	Tyr	Tyr	Ile	Pro
31	Met	Tyr	Phe	Ala	Ala	Pro	Trp	Val	Ile	Ala	His	Gly	Tyr	Arg	Gly
46	Thr	Ser	Asp	Gln	Tyr	Ser	Tyr	Gly	Trp	Phe	Leu	Asp	Asn	Val	Ser
61	Gln	Ser	Tyr	Thr	Asn	Thr	Gly	Asp	Asp	Ala	Trp	Ala	Gly	Gln	Lys
76	Asp	Leu	Ala	Tyr	Met	Gly	Ala	Gln	Cys	Gly	Pro	Phe	Asp	Gln	His
91	Phe	Val	Tyr	Glu	Ala	Gly	Asp	Gly	Leu	Glu	Asp	Val	Val	Thr	Ala
106	Phe	Ser	Tyr	Leu	Gln	Gly	Lys	Glu	Tyr	Glu	Asn	Gln	Gly	Leu	Asn
121	Ile	Arg	Ser	Ala	Met	Pro	Pro	Lys	Tyr	Val	Phe	Gly	Phe	Phe	Gln
136	Gly	Val	Phe	Gly	Ala	Thr	Ser	Leu	Leu	Arg	Asp	Asn	Leu	Pro	Ala
151	Gly	Glu	Asn	Asn	Val	Ser	Leu	Glu	Glu	Ile	Val	Glu	Gly	Tyr	Gln
166	Asn	Gln	Asn	Val	Pro	Phe	Glu	Gly	Leu	Ala	Val	Asp	Val	Asp	Met
181	Gln	Asp	Asp	Leu	Arg	Val	Phe	Thr	Thr	Arg	Pro	Ala	Phe	Trp	Thr
196	Ala	Asn	Lys	Val	Gly	Glu	Gly	Gly	Asp	Pro	Asn	Asn	Lys	Ser	Val
211	Phe	Glu	Trp	Ala	His	Asp	Arg	Gly	Leu	Val	Cys	Gln	Thr	Asn	Val
226	Thr	Cys	Phe	Leu	Lys	Asn	Glu	Lys	Asn	Pro	Tyr	Glu	Val	Asn	Gln
241	Ser	Leu	Arg	Glu	Lys	Gln	Leu	Tyr	Thr	Lys	Ser	Asp	Ser	Leu	Asp
256	Asn	Ile	Asp	Phe	Gly	Thr	Thr	Pro	Asp	Gly	Pro	Ser	Asp	Ala	Tyr
271	Ile	Gly	His	Leu	Asp	Tyr	Gly	Gly	Gly	Val	Glu	Cys	Asp	Ala	Leu
286	Phe	Pro	Asp	Trp	Gly	Arg	Pro	Asp	Val	Ala	Gln	Trp	Trp	Gly	Asp

301 Asn Tyr Lys Lys Leu Phe Ser Ile Gly Leu Asp Phe Val Trp Gln  
 316 Asp Met Thr Val Pro Ala Met Met Pro His Arg Leu Gly Asp Pro  
 331 Val Gly Thr Asn Ser Gly Glu Thr Ala Pro Gly Trp Pro Asn Asp  
 346 Lys Asp Pro Ser Asn Gly Arg Tyr Asn Trp Lys Ser Tyr His Pro  
 361 Gln Val Leu Val Thr Asp Met Arg Tyr Asp Asp Tyr Gly Arg Asp  
 376 Pro Ile Val Thr Gln Arg Asn Leu His Ala Tyr Thr Leu Cys Glu  
 391 Ser Thr Arg Arg Glu Gly Ile Val Gly Asn Ala Asp Ser Leu Thr  
 406 Lys Phe Arg Arg Ser Tyr Ile Ile Ser Arg Gly Gly Tyr Ile Gly  
 421 Asn Gln His Phe Gly Gly Met Trp Val Gly Asp Asn Ser Ser Thr  
 436 Glu Asp Tyr Leu Ala Met Met Val Ile Asn Val Ile Asn Met Asn  
 451 Met Ser Gly Val Pro Leu Val Gly Ser Asp Ile Gly Gly Phe Thr  
 466 Glu His Asp Lys Arg Asn Pro Cys Thr Pro Asp Leu Met Met Arg  
 481 Phe Val Gln Ala Gly Cys Leu Leu Pro Trp Phe Arg Asn His Tyr  
 496 Asp Arg Trp Ile Glu Ser Lys Lys His Gly Lys Asn Tyr Gln Glu  
 511 Leu Tyr Met Tyr Arg Asp His Leu Asp Ala Leu Arg Ser Phe Val  
 526 Glu Leu Arg Tyr Arg Trp Gln Glu Val Leu Tyr Thr Ala Met Tyr  
 541 Gln Asn Ala Leu Asn Gly Lys Pro Ile Ile Lys Thr Val Ser Met  
 556 Tyr Asn Asn Asp Met Asn Val Lys Asp Ala Gln Asn Asp His Phe

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGTTTTCAA	CCCTTGGCTT	TGTCGCACCT	AGTGCCTGG	GAGCCAGTAC	CTTCGTAGGG	60
GCGGAGGTCA	GGTCAAATGT	TCGTATCCAT	TCCGCTTTTC	CAGCTGTGCA	CACAGCTACT	120
CGCAAAACCA	ATCGCCTCAA	TGTATCCATG	ACCGCATTGT	CCGACAAACA	AACGGCTACT	180
GCGGGTAGTA	CAGACAATCC	GGACGGTATC	GACTACAAGA	CCTACGATTA	CGTCGGAGTA	240
TGGGGTTTCA	GCCCCCTCTC	CAACACGAAC	TGGTTTGCTG	CCGGCTCTTC	TACCCCGGGT	300
GGCATCACTG	ATTGGACGGC	TACAATGAAT	GTCAACTTCG	ACCGTATCGA	CAATCCGTCC	360
ATCACTGTCC	AGCATCCCGT	TCAGGTTGAG	GTCACGTCAT	ACAACAACAA	CAGCTACAGG	420
GTTTCGCTTCA	ACCCTGATGG	CCCTATTCTG	GATGTGACTC	GTGGGCCTAT	CCTCAAGCAG	480
CAACTAGATT	GGATTGGAAC	GCAGGAGCTG	TCAGAGGGAT	GTGATCCCGG	AATGACTTTC	540
ACATCAGAAG	GTTTTCTTGC	TTTTGAGACC	AAGGATCTAA	GCGTCATCAT	CTACGGAAAT	600
TTCAAGACCA	GAGTTACGAG	AAAGTCTGAC	GGCAAGGTCA	TCATGGAAAA	TGATGAAGTT	660
GGAAGTGCAT	CGTCCGGGAA	CAAGTGCCGG	GGATTGATGT	TCGTTGATAG	ATTATACGGT	720
AACGCTATCG	CTTCCGTCAA	CAAGAAGTTC	CGCAACGACG	CGGTCAAGCA	GGAGGGATTG	780
TATGGTGAG	GTGAAGTCAA	CTGTAAGTAC	CAGGACACCT	ACATCTTAGA	ACGCACTGGA	840
ATCGCCATGA	CAAATTACAA	CTACGATAAC	TTGAAGTATA	ACCAAGTGGG	CCTTAGACCT	900
CCGCATCATG	ATGGTGCCCT	CAACCCAGAC	TATTATATTC	CAATGACTA	CGCAGCACCT	960
TGGTTGATCG	TTAATGGATG	CGCCGGTACT	TCGGAGCAGT	ACTCGTATGG	ATGGTTCATG	1020
GACAAATGCT	CTCAATCTTA	CATGAATACT	GGAGATACTA	CCTGGAATTC	TGGACAAGAG	1080
GACCTGGCAT	ACATGGGCGC	GCAGTATGGA	CCATTTGACC	AACATTTTGT	TTACGGTGCT	1140
GGGGGTGGGA	TGGAATGTGT	GGTCACAGCG	TTCTCTCTTC	TACAAGGCAA	GGAGTTCGAG	1200
AACCAAGTTC	TCAACAACCG	TTCAGTAATG	CCTCCGAAAT	ACGTCTTTGG	TTTCTCCAG	1260
GGTGTTTTCG	GGACTTCTTC	CTTGTGTAGA	GCGCATATGC	CAGCAGGTGA	GAACAACATC	1320
TCAGTCGAAG	AAATTGTAGA	AGGTTATCAA	AACAACAATT	TCCCTTTTGA	GGGGCTCGCT	1380
GTGGACGTGG	ATATGCAAGA	CAACTTGGCG	GTGTTACCA	CGAAGGGCGA	ATTTTGGACC	1440
GCAAAACAGG	TGGGTACTGG	CGGGGATCCA	AACAACCGAT	CGGTTTTTGA	ATGGGCACAT	1500
GACAAAGGCC	TTGTTTGTCA	GACAAATATA	ACTTGTCTCC	TGAGGAATGA	TAACGAGGGG	1560
CAAGACTACG	AGGTCAATCA	GACGTTAAGG	GAGAGGCAGT	TGTACACGAA	GAACGACTCC	1620
CTGACGGGTA	CGGATTTTGG	AATGACCGAC	GACGGCCCCA	GCGATGCGTA	CATCGGTGAT	1680
CTGGACTATG	GGGGTGGAGT	AGAATGTGAT	GCACTTTTTC	CAGACTGGGG	ACGGCCTGAC	1740
GTGGCCGAAT	GGTGGGGAAA	TAAGTATAAG	AAACTGTTCA	GCATTTGGTCT	CGACTTCGTC	1800
TGGCAAGACA	TGACTGTTCC	AGCAATGATG	CCGCACAAAA	TTGGCGATGA	CATCAATGTG	1860
AAACCGGATG	GGAAATGGCC	GAATGCGGAC	GATCCGTCCA	ATGGACAATA	CAACTGGAAG	1920
ACGTACCATC	CCCAAGTGCT	TGTAAGTATG	ATGCGTTATG	AGAATCATGG	TCGGGAACCG	1980
ATGGTCACTC	AACGCAACAT	TCATGCGTAT	ACACTGTGCG	AGTCTACTAG	GAAGGAAGGG	2040
ATCGTGGAAA	ACGCAGACAC	TCTAACGAAG	TTCCGCCGTA	GCTACATTAT	CAGTCGTGGT	2100
GGTTACATTG	GTAACAGCA	TTTCGGGGGT	ATGTGGGTGG	GAGACAATC	TACTACATCA	2160

AACTACATCC	AAATGATGAT	TGCCAACAAT	ATTAACATGA	ATATGTCTTG	CTTGCCCTCTC	2220
GTCGGCTCCG	ACATTGGAGG	ATTCACCTCA	TACGACAATG	AGAATCAGCG	AACGCCGTGT	2280
ACCGGGGACT	TGATGGTGAG	GTATGTGCAG	GCGGGCTGCC	TGTTGCCGTG	GTTCCAGGAAC	2340
CACTATGATA	GGTGGATCGA	GTCCAAGGAC	CACGGAAAGG	ACTACCAGGA	GCTGTACATG	2400
TATCCGAATG	AAATGGATAC	GTTGAGGAAG	TTCGTTGAAT	TCCGTTATCG	CTGGCAGGAA	2460
GTGTTGTACA	CGGCCATGTA	CCAGAATGCG	GCTTTTCGGAA	AGCCGATTAT	CAAGGCTGCT	2520
TCGATGTACA	ATAACGACTC	AAACGTTCCG	AGGGCCGAGA	ACGATCATT	CCTTCTTGGT	2580
GGACATGATG	GATATCGCAT	TCTGTGCGCG	CCTGTTGTGT	GGGAGAATTC	GACCGAACGC	2640
GAATTGTACT	TGCCCGTGCT	GACCCAATGG	TACAAATTCG	GTCGCCACTT	TGACACCAAG	2700
CCTCTGGAAG	GAGCGATGAA	CGGAGGGGAC	CGAATTTACA	ACTACCCTGT	ACCGCAAAGT	2760
GAATCACCAA	TCTTCGTGAG	AGAAGGTGCG	ATTCTCCCTA	CCCCTACAC	GTTGAACGGT	2820
GAAAAACAA	CATTGAACAC	GTACACGGAC	GAAGATCCGT	TGGTGTGGA	AGTATTCCCC	2880
CTCGGAAACA	ACCGTGCCGA	CGGTATGTGT	TATCTTGATG	ATGGCGGTGT	GACCACCAAT	2940
GCTGAAGACA	ATGGCAAGTT	CTCTGTGCTC	AAGGTGGCAG	CGGAGCAGGA	TGGTGTACG	3000
GAGACGATAA	CGTTTACGAA	TGATTGCTAT	GAGTACGTTT	TCGGTGGACC	GTTCTACGTT	3060
CGAGTGGCG	GCGCTCAGTC	GCCGTGGAAC	ATCCACGTGT	CTTCTGGAGC	GGGTTCTCAG	3120
GACATGAAGG	TGAGCTCTGC	CACTCCAGG	GCTGCGCTGT	TCAATGACGG	GGAGAACGGT	3180
GATTTCTGGG	TTGACCAGGA	GACAGATTCT	CTGTGGCTGA	AGTTGCCCAA	CGTTGTTCTC	3240
CCGGACGCTG	TGATCACAA	TACCTAA				3267

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3276 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

ATGATCCAA	CCCTCACCTT	CGTGGCGCCT	AGTGCCTAG	GGGCCAGAAC	TTTACGTGT	60
GTGGGCATTT	TTAGGTCACA	CATTCTTATT	CATTTCGGTTG	TTCCAGCGGT	GCGTCTAGCT	120
GTGCGCAAAA	GCAACCGCCT	CAATGTATCC	ATGTCCGCTT	TGTTTCGACAA	ACCGACTGCT	180
GTTACTGGAG	GGAAGGACAA	CCCGGACAAT	ATCAATTACA	CCACTTATGA	CTACGTCCCT	240
GGTGGCGCT	TCGACCCCTC	CAGCAATACG	AACTGGTTTG	CTGCCGGATC	TTCCACTCCC	300
GTGCAATTTG	ACGACTGGAC	GCGGACAATG	AATGTGAACT	TCGACCGTAT	GACAAATCCA	360
TCCTTCACTC	TCGAGAAACC	GGTTCAGGTT	CAGGTCACGT	CATACAAGAA	CAATTGTTTC	420
AGGGTTCGCT	TCAACCCCTGA	TGGTCCCTATT	CGCGATGTGG	ATCGTGGGCC	TATCCTCCAG	480
CAGCAACTAA	ATTGGATCCG	GAAGCAGGAG	CAGTCGAAGG	GGTGTTGATCC	TAAGATGGGC	540
TTCAAAAAG	AAGGTTTCTT	GAAATTTGAG	ACCAAGGATC	TGAACGTTAT	CATATATGGC	600
AATTTTAAAG	CTAGAGTTAC	GAGGAAGAGG	GATGGAAAAG	GGATCATGGA	GAATAATGAA	660
GTGCCGGCAG	GATCGTTAGG	GAACAAGTGC	CGGGGATTGA	TGTTTGTCTGA	CAGGTTGTAC	720
GGCACTGCCA	TCGCTTCCGT	TAATGAAAAT	TACCGCAACG	ATCCCGACAG	GAAGAGGGG	780
TTCTATGGTG	CAGGAGAAGT	AAACTGCGAG	TTTTGGGACT	CCGAACAAAA	CAGGAACAAG	840
TACATCTTAG	AACGAACTGG	AATCGCCATG	ACAAATTACA	ATTATGACAA	CTATAACTAC	900
AACCACTCAG	ATCTTATTGC	TCCAGGATAT	CCTCCGACC	CGAACTTCTA	CATTCCCATG	960
TATTTTGCAG	CACCTTGGGT	AGTTGTTAAG	GGATGCAGTG	GCAACAGCGA	TGAACAGTAC	1020
TCGTACGGAT	GGTTTATGGA	TAATGTCCTC	CAAACTTACA	TGAATACTGG	TGGTACTTCC	1080
TGGAACCTGTG	GAGAGGAGAA	CTTGGCATA	ATGGGAGCAC	AGTGCCTGCC	ATTTGACCAA	1140
CATTTTGTGT	ATGGTGATGG	AGATGGTCTT	GAGGATGTTG	TCCAAGCGTT	CTCTCTTCTG	1200
CAAGGCAAAAG	AGTTTGAGAA	CCAAGTCTG	AACAAACGTG	CCGTAATGCC	TCCGAAATAT	1260
GTGTTTGGTT	ACTTTCAGGG	AGTCTTTGGG	ATTGCTTCCCT	TGTTGAGAGA	GCAAAGACCA	1320
GAGGGTGGTA	ATAACATCTC	TGTTCAAGAG	ATTGTCGAAG	GTTACCAAAG	CAATAACTTC	1380
CCTTTAGAGG	GGTTAGCCGT	AGATGTGGAT	ATGCAACAAG	ATTTGCGCGT	GTTCAACCAG	1440
AAGATTGAAT	TTTGGACGGC	AAATAAGGTA	GGCACCAGGG	GAGACTCGAA	TAACAAGTGC	1500
GTGTTTGAAT	GGGCACATGA	CAAAGGCCCT	GTATGTCAGA	CGAATGTTAC	TTGCTTCTTG	1560
AGAAACGACA	ACGGCGGGGC	AGATTACGAA	GTCAAATCAGA	CATTGAGGGA	GAAGGGTTTG	1620
TACACGAAGA	ATGACTCACT	GACGAACACT	AACTTCGGAA	CTACCAACGA	CGGGCCGAGC	1680
GATGCGTACA	TTGGACATCT	GGACTATGGT	GGCGGAGGGA	ATTGTGATGC	ACTTTTCCCA	1740
GACTGGGGTC	GACCGGGTGT	GGCTGAATGG	TGGGGTGATA	ACTACAGCAA	GCTCTTCAA	1800
ATTGGTCTGG	ATTTCTGCTG	GCAAGACATG	ACAGTTCCAG	CTATGATGCC	ACACAAAGTT	1860
GGCGACGCAG	TCGATACGAG	ATCACCTTAC	GGCTGGCCGA	ATGAGAATGA	TCCCTCGAAC	1920
GGACGATACA	ATTGGAATC	TTACCATCCA	CAAGTTCTCG	TAAGTATGAT	GCGATATGAG	1980
AATCATGGAA	GGGAACCGAT	GTTCACTCAA	CGCAATATGC	ATGCGTACAC	ACTCTGTGAA	2040

TCTACGAGGA	AGGAAGGGAT	TGTTGCAAA	GCAGACACTC	TAACGAAGTT	CCGCCGAGT	2100
TATATTATCA	GTCGTGGAGG	TTACATTGGC	AACCAGCATT	TTGGAGGAAT	GTGGGTTGGA	2160
GACAACTCTT	CCTCCCAAAG	ATACCTCCAA	ATGATGATCG	CGAACATCGT	CAACATGAAC	2220
ATGCTTGCC	TTCCACTAGT	TGGGTCCGAC	ATTGGAGGTT	TTACTTCGTA	TGATGGACGA	2280
AACGTGTGTC	CCGGGGATCT	AATGGTAAGA	TTCGTGCAGG	CGGGTTGCTT	ACTACCGTGG	2340
TTCAGAAACC	ACTATGGTAG	GTTGGTCGAG	GGCAAGCAAG	AGGGAAAAATA	CTATCAAGAA	2400
CTGTACATGT	ACAAGGACGA	GATGGCTACA	TTGAGAAAAT	TCATTGAATT	CCGTTACCGC	2460
TGGCAGGAGG	TGTTGTACAC	TGCTATGTAC	CAGAATGCCG	CTTTCGGGAA	ACCGATTATC	2520
AAGGCAGCTT	CCATGTACGA	CAACGACAGA	AACGTTCCGG	GCCGACAGGA	TGACCACTTC	2580
CTTCTCGGCG	GACACGATGG	ATATCGTATT	TTGTGTGCAC	CTGTTGTGTG	GGAGAATACA	2640
ACCAGTCCGC	ATCTGTACTT	GCCTGTGCTG	ACCAAATGGT	ACAAATTCGG	CCCTGACTAT	2700
GACACCAAGC	GCCTGGATTG	TGCGTTGGAT	GGAGGGCAGA	TGATTAAGAA	CTATTCTGTG	2760
CCACAAGCG	ACTCTCCGAT	ATTTGTGAGG	GAAGGAGCTA	TTCTCCCTAC	CCGCTACACG	2820
TTGGACGGTT	CGAACCAAGT	AATGAACAGT	TACACAGACA	AAGACCCGTT	GGTGTTTGAG	2880
GTATTCCCTC	TTGGAAACAA	CCGTGCCGAC	GGTATGTGTT	ATCTTGATGA	TGGCGGTATT	2940
ACTACAGATG	CTGAGGACCA	TGGCAAATTC	TCTGTTATCA	ATGTCGAAGC	CTTACGGAAA	3000
GGTGTACGA	CGACGATCAA	GTTTGCATAT	GACACTTATC	AATACGTATT	TGATGGTCCA	3060
TTCTACGTTG	GAATCGTAA	TCTTACGACT	GCATCAAAAA	TTAACGTGTC	TTCTGGAGCG	3120
GGTGAAGAGG	ACATGACACC	GACCTCTGCG	AACTCGAGGG	CAGCTTTGTT	CAGTGATGGA	3180
GGTGTGGAG	AATACTGGGC	TGACAATGAT	ACGTCTTCTC	TGTGGATGAA	GTTGCCAAAC	3240
CTGGTTCTGC	AAGACGCTGT	GATTACCATT	ACGTAG			3276

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGGCAGGAT	TTTCTGATCC	TCTCAACTTT	TGCAAAGCAG	AAGACTACTA	CAGTGTTCGG	60
CTAGACTGGA	AGGGCCCTCA	AAAAATCATT	GGAGTAGACA	CTACTCCTCC	AAAGAGCACC	120
AAGTTCGCCA	AAAACCTGGCA	TGGAGTGAAC	TTGAGATTCC	ATGATGGGAC	TTTAGGTGTG	180
GTTCAAGTTC	TTAGGCCGCTG	CGTTTGGAGG	GTTAGATACG	ACCCTGGTTT	CAAGACCTCT	240
GACGAGTATG	GTGATGAGAA	TACGAGGACA	ATTGTGCAAG	ATTATATGAG	TACTCTGAGT	300
AATAAATTGG	ATACTTATAG	AGGTCTTACG	TGGGAAACCA	AGTGTGAGGA	TTCGGGAGAT	360
TTCTTTACCT	TCTCATCCAA	GGTCACCGCC	GTTGAAAAAT	CCGAGCGGAC	CCGCAACAAG	420
GTCCGGCAGT	GCCTCAGAAT	TCACCTATGG	AAAAGCCCTT	TCCGCATCCA	AGTAGTGCCG	480
ACCTTTGACC	CTTTGAAGGA	TCCTTACCC	ATTCCAAATG	TAGCCGCAGC	CGAAGCCCGT	540
GTGTCCGACA	AGGTCGTTTG	GCAAACGTCT	CCCAAGACAT	TCAGAAAGAA	CCTGCATCCG	600
CAACACAAGA	TGCTAAAAGGA	TACAGTTCTT	GACATTGTCA	AACTGGGACA	TGGCGAGTAT	660
GTGGGGTGGG	GAGAGATGGG	AGGTATCCAG	TTTATGAAGG	AGCCAACATT	CATGAACTAT	720
TTTAACTTCG	ACAATATGCA	ATACCAGCAA	GTCTATGCC	AAGGTGCTCT	CGATTCTCGC	780
GAGCCACTGT	ACCACTCGGA	TCCCTTCTAT	CTTGATGTGA	ACTCCAACCC	GGAGCACAAG	840
AATATCACGG	CAACCTTTAT	CGATAACTAC	TCTCAAATTG	CCATCGACTT	TGGAAAGACC	900
AACTCAGGCT	ACATCAAGCT	GGGAACCAGG	TATGGTGGTA	TCGATTGTTA	CGGTATCAGT	960
GCGGATACCG	TCCCGGAAAT	TGTACGACTT	TATACAGGTC	TTGTTGGACG	TTCAAAGTTG	1020
AAGCCAGAT	ATATTCTCGG	GGCCCATCAA	GCCTGTTATG	GATACCAACA	GGAAAGTGAC	1080
TTGTATTCTG	TGGTCCAGCA	GTACCGTGAC	TGTAAATTTT	CACTTGACGG	GATTCACGTC	1140
GATGTCGATG	TTCAGGACGG	CTTCAGAACT	TTACCACCA	ACCCACACAC	TTCCCTAAC	1200
CCCAAAGAGA	TGTTTACTAA	CTTGAGGAAT	AATGGAATCA	AGTGCTCCAC	CAATATCACT	1260
CCTGTTATCA	GCATTAACAA	CAGAGAGGGT	GGATACAGTA	CCCTCCTTGA	GGGAGTTGAC	1320
AAAAAATACT	TTATCATGGA	CGACAGATAT	ACCGAGGGAA	CAAGTGGGAA	TGCGAAGGAT	1380
GTTCCGGTACA	TGTAACACGG	TGGTGGTAAT	AAGGTTGAGG	TGCATCTTAA	TGATGTTAAT	1440
GGTCCGGCAG	ACTTTAAAGA	CAACTATGAC	TTCCCCGCGA	ACTTCAACAG	CAAACAATAC	1500
CCCTATCATG	TGGTGTGAG	CTACGGTTAT	GGGAACGGTA	GTGCAGGTTT	TTACCCGGAC	1560
CTCAACAGAA	AGGAGGTTCC	TATCTGGTGG	GGAAATGCAGT	ACAAGTATCT	CTTCGATATG	1620
GGACTGGAA	TTGTGTGGCA	AGACATGACT	ACCCACAGAA	TCCACACATC	ATATGGAGAC	1680
ATGAAAGGGT	TGCCACCCCG	TCTACTCGTC	ACCTCAGACT	CCGTCACCAA	TGCCTCTGAG	1740
AAAAAGCTCG	CAATTTGAAAC	TTGGGCTCTC	TACTCTTACA	ATCTCCACAA	AGCAACTTGG	1800
CATGGTCTTA	GTCGTCTCGA	ATCTCGTAAG	AACAAACGAA	ACTTCATCCT	CGGGCGTGGG	1860
AGTTATGCCG	GAGCCTATCG	TTTTGCTGGT	CTCTGGACTG	GGGATAATGC	AAGTAACTGG	1920
GAATTCTGGA	AGATATCGGT	CTCTCAAGTT	CTTTCTCTGG	GCCTCAATGG	TGTGTGCATC	1980

GGGGGGTCTG	ATACGGGTGG	TTTGAACCC	TACCGTATG	CAAATGGGGT	CGAGGAGAAA	2040
TACTGTAGCC	CAGAGCTACT	CATCAGGTGG	TATACTGGTT	CATTCCCTCTT	GCCGTGGCTC	2100
AGGAACCATT	ATGTCAAAA	GGACAGGAAA	TGGTTCAGG	AACCATACTC	GTACCCCAAG	2160
CATCTTGAAA	CCCATCCAGA	ACTCGCAGAC	CAAGCATGGC	TCTATAAATC	CGTTTTGGAG	2220
ATCTGTAGGT	ACTATGTGGA	GCTTAGATAC	TCCCTCATCC	AACTACTTTA	CGACTGCATG	2280
TTTCAAAACG	TAGTCGACGG	TATGCCAATC	ACCAGATCTA	TGCTCTTGAC	CGATACTGAG	2340
GATACCACCT	TCTTCAACGA	GAGCCAAAAG	TTCTCGACA	ACCAATATAT	GGCTGGTGAC	2400
GACATTCTTG	TTGCACCCAT	CCTCCACAGT	CGCAAAGAAA	TTCCAGGGCA	AAACAGAGAT	2460
GTCTATCTCC	CTCTTTACCA	CACCTGGTAC	CCCTCAAATT	TGAGACCATG	GGACGATCAA	2520
GGAGTCGCTT	TGGGGAATCC	TGTCGAAGGT	GGTAGTGTCA	TCAATTATAC	TGCTAGGATT	2580
GTTGCACCCG	AGGATTATAA	TCTCTTCCAC	AGCGTGGTAC	CAGTCTACGT	TAGAGAGGGT	2640
GCCATCATCC	CGCAAATCGA	AGTACGCCAA	TGGACTGGCC	AGGGGGGAGC	CAACCCGATC	2700
AAGTTCAACA	TCTACCCTGG	AAAGGATAAG	GAGTACTGTA	CCTATCTTGA	TGATGGTGT	2760
AGCCGTGATA	GTGCGCCGGA	AGACCTCCCA	CAGTACAAAG	AGACCCACGA	ACAGTCGAAG	2820
GTTGAAGGCG	CGGAAATCGC	AAAGCAGATT	GGAAGAAGA	CGGGTTACAA	CATCTCAGGA	2880
ACCGACCCAG	AAGCAAAGGG	TTATCACCGC	AAAGTTGCTG	TCACACAAC	GTCAAAGAGC	2940
AAGACGGCTA	CTGTCACTAT	TGAGCCAAA	CACAATGGAT	ACGACCCTTC	CAAAGAGGTG	3000
GGTGATTATT	ATACCATCAT	TCTTTGGTAC	GCACCAGGTT	TCGATGGCAG	CATCGTCGAT	3060
GTGAGCAAGA	CGACTGTGAA	TGTTGAGGGT	GGGGTGGAGC	ACCAAGTTTA	TAAGAACTCC	3120
GATTTACATA	CGGTTGTTAT	CGACGTGAAG	GAGGTGATCG	GTACCACAAA	GAGCGTCAAG	3180
ATCATATGTA	CTGCCGCTTA	A				3201

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3213 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATGGCAGGAT	TATCCGACCC	TCTCAATTC	TGCAAAGCAG	AGGACTACTA	CGCTGCTGCC	60
AAAGGCTGGA	GTGGCCCTCA	GAAGATCATT	CGCTATGACC	AGACCCTCC	TCAGGGTACA	120
AAAGATCCGA	AAAGCTGGCA	TGCGGTAAAC	CTTCCTTCG	ATGACGGGAC	TATGTGTGTA	180
GTGCAATTCG	TCAGACCCTG	TGTTTGGAGG	GTTAGATATG	ACCCAGTGT	CAAGACTTCT	240
GATGATACG	GCGATTGAGAA	TACGAGGACT	ATTGTACAAG	ACTACATGAC	TACTCTGGTT	300
GGAAACTTGG	ACATTTTCAG	AGGTCTTACG	TGGGTTTCTA	CGTTGGAGGA	TTCGGGCGAG	360
TACTACACCT	TCAAGTCCGA	AGTCACTGCC	GTGGACGAAA	CCGAACGGAC	TCGAAACAAG	420
GTCGGCGCAG	GCCTCAAGAT	TTACCTATGG	AAAAATCCCT	TTGCGATCCA	GGTAGTGCCT	480
CTCTTGACCC	CCCTGGTGGG	CCCTTTCCCC	ATTCCCAACG	TAGCCAATGC	CACAGCCCGT	540
GTGGCCGACA	AGGTTGTTTG	GCAGACGTCC	CCGAAGACGT	TCAGGAAAAA	CTTGCATCCG	600
CAGCATAAGA	TGTTGAAGGA	TACAGTCTT	GATATTATCA	AGCCGGGGCA	CGGAGAGTAT	660
GTGGGTTGGG	GAGAGATGGG	AGGCATCGAG	TTTATGAAGG	AGCCAACATT	CATGAATTAT	720
TTCAACTTTG	ACAATATGCA	ATATCGCAG	GTCTATGCAC	AAGGCGCTCT	TGATAGTCGT	780
GAGCCGTTGT	ATCACTCTGA	TCCCTTCTAT	CTCGACGTGA	ACTCCAACCC	AGAGCACAAG	840
AACATTACGG	CAACCTTTAT	CGATAACTAC	TCTCAGATTG	CCATCGACTT	TGGGAAGACC	900
AACTCAGGCT	ACATCAAGCT	GGGTACCAGG	TATGGCGGTA	TCGATTGTTA	CGGTATCAGC	960
GCGGATACCG	TCCCGGAGAT	TGTGCGACTT	TATACTGGAC	TTGTTGGGCG	TTCGAAGTTG	1020
AAGCCAGGT	ATATTCTCGG	AGCCACCAA	GCTTGTATG	GATACCAGCA	GGAAAGTGAC	1080
TTGCATGCTG	TTGTTCAAGCA	GTACCGTGAC	ACCAAGTTTC	CGTTGATGG	GTTGCATGTC	1140
GATGTCGACT	TTCAGGACAA	TTTCAGAACG	TTTACCACTA	ACCCGATTAC	GTTCCCTAAT	1200
CCCAAAGAAA	TGTTTACCAA	TCTAAGGAAC	AATGGAATCA	AGTGTTCAC	CAACATCACC	1260
CCTGTTATCA	GTATCAGAGA	TCGCCGAAT	GGGTACAGTA	CCCTCAATGA	GGGATATGAT	1320
AAAAAGTACT	TCATCATGGA	TGACAGATAT	ACCGAGGGGA	CAAGTGGGGA	CCCGCAAAT	1380
GTTTCGATACT	CTTTTTACGG	CGGTGGGAAC	CCGGTTGAGG	TTAACCTAA	TGATGTTTGG	1440
GCTCGGCCAG	ACTTTGGAGA	CAATTATGAC	TTCCCTACGA	ACTTCAACTG	CAAAGACTAC	1500
CCCTATCATG	TGGGTGTGAG	TTACGGATAT	GGGAATGGCA	CTCCAGGTTA	CTACCCTGAC	1560
CTTAACAGAG	AGGAGGTTTC	TATCTGGTGG	GGATTGCAGT	ACGAGTATCT	CTTCAATATG	1620
GGACTAGAGT	TTGTATGGCA	AGATATGACA	ACCCAGCGA	TCCATTCATC	ATATGGAGAC	1680
ATGAAAGGGT	TGCCACCCG	TCTGCTCGTC	ACCGCCGACT	CAGTTACCAA	TGCCTCTGAG	1740
AAAAAGCTCG	CAATTGAAAG	TTGGGCTCTT	TACTCCTACA	ACCTCCATAA	AGCAAACCTTC	1800
CACGGTCTTG	GTCGTCTTGA	GTCTCGTAAG	AACAAACGTA	ACTTCATCCT	CGGACGTGGT	1860
AGTTACGCCG	GTCCCTATCG	TTTTGCTGGT	CTCTGGACTG	GAGATAACGC	AAGTACGTGG	1920
GAATTCGGA	AGATTTCCGT	CTCCCAAGTT	CTTTCTCTAG	GTCTCAATGG	TGTGTGTATA	1980



```

GCGGGGTCTG ATACGGGTGG TTTTGAGCCC GCACGTA CTG AGATTGGGGA GGAGAAATAT 2040
TGCAGTCCGG AGCTACTCAT CAGGTGGTAT ACTGGATCAT TCCTTTTGCC ATGGCTTAGA 2100
AACCCTACG TCAGAAGGA CAGGAAATGG TTCCAGGAAC CATACGCGTA CCCCAAGCAT 2160
CTTGAACCC ATCCAGAGCT CGCAGATCAA GCATGGCTTT ACAATCTGT TCTAGAAATT 2220
TGCAGATACT GGGTAGAGCT AAGATATTCC CTCATCCAGC TCCTTTACGA CTGCATGTT 2280
CAAAACGTGG TCGATGGTAT GCCACTTGCC AGATCTATGC TCTTGACCGA TACTGAGGAT 2340
ACGACCTTCT TCAATGAGAG CCAAAGTTC CTCGATAACC AATATATGGC TGGTGACGAC 2400
ATCCTTGTAG CACCCATCCT CCACAGCCGT AACGAGGTT CCGGAGAGAA CAGAGATGTC 2460
TATCTCCCT TATTCCACAC CTGGTACCCC TCAAAGTTGA GACCGTGGGA CGATCAGGGA 2520
GTCGCTTTAG GGAATCCTGT CGAAGGTGGC AGCGTTATCA ACTACACTGC CAGGATTGTT 2580
GCCCCAGAGG ATTATAATCT CTTCCACAAC GTGGTGCCGG TCTACATCAG AGAGGGTGCC 2640
ATCATTCGCG AAATTCAGGT ACGCCAGTGG ATTGGCGAAG GAGGGCCTAA TCCCATCAAG 2700
TTCAATATCT ACCTGGAAA GGACAAGGAG TATGTGACGT ACCTTGATGA TGGTGTAGC 2760
CGCGATAGTG CACCAGATGA CCTCCCGCAG TACCGCGAGG CCTATGAGCA AGCGAAGGTC 2820
GAAGGCAAA ACCTCCAGAA GCAACTTGGC GTCAATCAAG GGAATAAGAC TAATGACTTC 2880
TCCGCTCCG GGATTGATA GGAGGCAAAG GGTATCACC GCAAAGTTT TATCAAACAG 2940
GAGTCAAAG ACAAGACCCG TACTGTCCG ATTGAGCCAA AACACAACGG ATACGACCCC 3000
TCTAAGGAAG TTGGTAATTA TTATACCATC ATCTTTGGT ACGCACCAGG CTTTGACGGC 3060
AGCATCGTCG ATGTGAGCCA GGCGACCGTG AACATCGAGG GCGGGGTGGA ATGCGAAATT 3120
TTCAAGAAAC CCGGCTTGA TACGGTTGTA GTCAACGTGA AAGAGGTGAT CGGTACCACA 3180
AAGTCCGTCA AGATCACTTG CACTACCGCT TAG 3213

```

SEQ. ID. NO. 11

```

SEQUENCE TYPE: NUCLEIC ACID
MOLECULE TYPE: DNA (GENOMIC)
ORIGINAL SOURCE: ALGAL
SEQUENCE LENGTH: 3279 BP
STRANDEDNESS: DOUBLE
SEQUENCE:

```

```

          10          20          30          40          50          60
1  ATGTTTCTTA  CCCTGACCTT  CATAGCGCCC  AGCGCGCTGG  CCGCCAGCAC  CTTTGTGGGC
61 GCGGATATCC  GATCGGGCAT  TCGCATTCAA  TCCGCTCTTC  CGGCCGTGCG  CAACGCTGTG
121 CGCAGGAGCA  AACATTACAA  TGTATCCATG  ACCGCATTGT  CTGACAAGCA  AACCGCTATC
181 AGTATTGGCC  CTGACAATCC  GGACGGTATC  AACTACAAA   ACTACGATTA  CATCCCTGTA
241 GCGGGCTTTA  CGCCCTCTC  CAACACCAAC  TGGTATGCTG  CCGGCTCTTC  CACTCCGGGC
301 GGCATCACCG  ACTGGACCCG  TACCATGAAT  GTCAAATTCG  ACCGCATTGA  CAATCCGTGG
361 TACTCCAATA  ACCATCCTGT  TCAGATTCAG  GTCACGTCGT  ACAACAACAA  CAGCTTCAGG
421 ATTGCGTTCA  ACCCTGATGG  CCCCATTCGT  GACGCTCTCT  GAGGACCTAT  CCTGAAACAG
481 CAACTCACTT  GGATTCGAAA  CCAGGAGCTG  GCGCAGGGAT  GTAATCCGAA  CATGAGCTTC
541 TCTCCTGAAG  GTTTTTGTG  TTTTGAAACC  AAAGACCTAA  ACGTTATAAT  CTACGGCAAC
601 TGCAAGATGA  GAGTACGAA  GAAGGATGGC  TACCTCGTCA  TGGAGAATGA  CGAGTGCAAC
661 TCGCAATCAG  ATGGCAATAA  GTGTAGAGGA  TTGATGTACG  TTGACCGGCT  ATACGGTAAT
721 GCTATTGCTT  CCGTACAAAC  GAATTTTAC  AAAGACTT   CTCGGAACGA  GAAATCTAT
781 GGTGCAGGTG  AAGTCAACTG  TCGCTATGAG  GAGCAGGGTA  AGGCGCCGAC  TTATGTTCTA
841 GAACGCTCTG  GACTCGCCAT  GACCAATTAC  AATTACGACA  ACTTGAACTA  CAACCAACCA
901 GACGTGCTTC  CTCCAGGTTA  TCCCGACCAT  CCCAACTACT  ACATTCCAAT  GACTACGCA
961 GCACCGTGGT  TGGTCGTTCA  GGGATGCGCG  GGGACATCGA  AGCAATACTC  GTACGGTTGG
1021 TTTATGGACA  ATGTCTCTCA  GTCGTACATG  AACACTGGAG  ATACGGCGTG  GAACTGCGGA
1081 CAGGAAAACC  TGGCATACAT  GGGCGCGCAA  TACGGCCAT  TTGATCAGCA  CTTTGTGTAT
1141 GGTGATGGAG  ATGGCCTTGA  AGATGTGCTC  AAAGCGTTCT  CCTTCTTCA  AGGAAAGGAG
1201 TTCGAAGACA  AAAAATCAA  CAAGCGTTCT  GTAATGCCTC  CGAAGTACGT  GTTTGGTTTC
1261 TTCAGGGTG  TTTTCGGTGC  ACTTTCCTG  TTGAAGCAGA  ATCTGCCTGC  CGGAGAGAAC
1321 AACATCTCAG  TGCAAGAGAT  TGTGGAGGGT  TACCAGGATA  ACGACTACCC  CTTTGAAGGG
1381 CTCGCGGTAG  ATGTTGATAT  GCAAGATGAT  CTGCGAGTGT  TTAATACCAA  ACCAGAATAT
1441 TGGTCGGCAA  ACATGGTAGG  CGAAGGCGGT  GATCCTAATA  ACAGATCAGT  CTTTGAATGG
1501 GCACATGACA  GGGGCCTTGT  CTGTGAGACG  AACGTAACCT  GCTTCTTGAG  GAACGATAAC
1561 AGTGGGAAAC  CATACGAAGT  GAATCAGACA  TTGAGGGAGA  AACAGTTGTA  TACGAAGAAT
1621 GATTCTTGA  ACAACACCGA  TTTTGGAACT  ACCTCGGATG  GGCCTGGCGA  TCGTACATT
1681 GGACATTTGG  ACTATGGTGG  TGGAGTGGAG  TGTGATGCAA  TCTTCCGAGA  CTGGGGTCTG
1741 CCAGACGTGG  CTCAATGGTG  GGGAGAAAAC  TACAAGAAGC  TGTTCCAGAT  TGGTCTCGAT
1801 TTCGTGTGGC  AGGATATGAC  GGTACCTGCG  ATGATGCCGC  ACCGACTCGG  TGATGCTGTC
1861 ACAAATAATT  CCGGTAGTTC  GGCCTGGGCG  TGGCCGAATG  AGAACGATCC  ATCCAACGGA
1921 CGATACAAC  TCAATCTTGA  TCAATCTTGA  TCAATCTTGA  TCAATCTTGA  TCAATCTTGA
1981 GAGTATGGAA  GGAACCCGAT  GGTGTCTCAA  CGCAACATTC  ACGCTACAC  TCTTTGTGAA
2041 TCTACCAGAC  GGGAGGGAAT  TGTGGGAAAC  GCAGACAGTT  TGACCAAGTT  CCGCCGCGAGT

```

```

2101 TACATCATCA GTCGAGGAGG TTACATCGGT AACAGCATT TCGGAGGGAT GTGGGTGGG
2161 GACAACAGTG CCACAGAATC CTACCTCCAA ATGATGTTGG CGAACATTAT CAACATGAAT
2221 ATGTCGTGCC TCCCCTAGT TGGCTCTGAT ATTGGCGGGT TCACCCAGTA CAATGATGCG
2281 GGCACCCAA CCCCAGGGA TTTGATGGTA AGATTCGTGC AGGCTGGCTG TCTGCTACCG
2341 TGGTTCAGAA ACCACTATGA CAGGTGGATT GAGTCCAAGA AGCACGGGAA GAAATACCAG
2401 GAGTTATACA TGTACCCGGG GCAAAAAGGAT ACGTTGAAGA AGTTCGTTGA ATTCCGCTAC
2461 CGCTGGCAGG AGGTTTTGTA CACAGCCATG TACCAAAATG CTACCACTGG AGAGCCGATC
2521 ATCAAGGCGG CGCCCATGTA CAACAACGAC GTC AACGTGT ATAAATCGCA GAATGATCAT
2581 TTCCTTCTCG GTGGACATGA CGGCTATCGT ATTCTCTGCG CACCTGTTGT GCGCGAAAAT
2641 GCGACAAGTC GCGAAGTGT CCTGCCTGTG TATAGCAAGT GGTTCAAAT CGGACCGGAC
2701 TTTGACACTA AGCCCTTGGG AAATGAGATT CAAGGAGGTC AGACGCTTTA TAATTACGCT
2761 GCACCGTGA ACGATTCGCC GATATTTGTG AGGGAAGGGA CTATTCTTCC GACACGGTAC
2821 ACCGTTGACG GTGTGAACAA ATCTATCAAC ACGTACACAG ACAATGATCC GCTTGATTTT
2881 GAGCTGTTC CTCTCGAAAA CAACCAGGCG CATGGCTTGT TCTATCATGA TGATGGCGGT
2941 GTACCACCA ACGTGAAGA CTTGGCAAG TATTCTGTGA TCAGTGTGAA GGCCTGCGAG
3001 GAAGGTTCTC AAATGAGTGT CAAGTTTGTG AATGAAGTTT ATGAACACCA ATGGGGAGCA
3061 TCGTGTATG TTCGTGTTG TAATATGGGT GCTCCGTCTA ACATCAACGT ATCTTCTCAG
3121 ATTGGTCAAC AGGACATGCA ACAGAGCTCC GTGAGTTCCA GGGCGCAAAT GTTCACTAGT
3181 GCTAACGATG GCGAGTACTG GGTGACCAG AGCACGAACT CGTTGTGGCT CAAGTTGCC
3241 GGTGCAAGT TCCAAGACGC TGGCATCACT GTTCGTTGA
    
```

SEQ. ID. NO. 12

SEQUENCE TYPE: NUCLEIC ACID  
 MOLECULE TYPE: DNA (GENOMIC)  
 ORIGINAL SOURCE: ALGAL  
 SEQUENCE LENGTH: 1712 BP  
 STRANDEDNESS: DOUBLE  
 SEQUENCE:

```

          10      20      30      40      50      60
1  ATGACAAACT ATAATTATGA CAATTTGAAC TACAATCAAC CGGACCTCAT CCCACCTGGC
61 CATGATTCAG ATCCTGACTA CTATATTCCG ATGTACTTTG CGGCACCATG GGTGATCGCA
121 CATGGATATC GTGGCACCAG CGACCAGTAC TCTTATGGAT GGTTTTTTGA CAATGTATCC
181 CAGTCTACA CAAACTGCG CGATGATGCA TGGGCTGGTC AGAAGGATTT GGCCTACATG
241 GGGGCACAAT GTGGGCCTTT CGATCAACAT TTTGTGATG AGGCTGGAGA TGGACTTGAA
301 GCGTGTGTGA CCGCATTCTC TTATTTGCAA GGCAAGGAAT ATGAGAACCA GGGACTGAAT
361 ATACGTTCTG CAATGCCTCC GAAGTACGTT TTCGGATTTT TCCAAGGCGT ATTCCGAGCC
421 ACATCGCTGC TAAGGGACAA CTTACCTGCC GGCGAGAACA ACGTCTCTTT GGAAGAAATT
481 GTTGAAGGAT ATCAAAATCA GAACGTGCCA TTTGAAGGTC TTGCTGTGGA TGTGATATG
541 CAAGATGACT TGAGAGTGT CACTACGAGA CCAGCGTTTT GGACGGCAAA CAAGGTGGGG
601 GAAGGCGGTG ATCCAACAA CAAGTCAGTG TTTGAGTGGG CACATGACAG GGCCTTGTC
661 TGCCAGACGA ATGTAACCTG CTTCTTGAAG AACGAGAAAA ATCCTTACGA AGTGAATCAG
721 TCATTGAGGG AGAAGCAGTT GTATACGAAG AGTGATTCCT TGGACAACAT TGATTTTGA
781 ACTACTCCAG ATGGGCTAG CGATGCGTAC ATTGGACACT TAGACTACGG TGGTGGTGTG
841 GAGTGTGATG CACTATTCCC AGACTGGGGT CGACCAGACG TGGCTCAATG GTGGGGCGAT
901 AACTACAAGA AACTATTGAG CATTGGTCTC GATTTGCTCT GGCAAGATAT GACGGTACCT
961 GCGATGATGC CGCACCAGCT CGGTGACCCT GTCGGCACA ATTCCGGTGA GACGGCGCCG
1021 GGCTGGCCGA ATGATAAGGA TCCATCCAAC GGACGATACA ATTTGGAAGT TTACCATCCG
1081 CAAGTGCTCG TGAAGTACAT GAGGTATGAC GATTACGGAA GAGATCCCAT TGTACGCAA
1141 CGCAATCTCC ATGCTACAC TCTTTGTGAG TCTACTAGGA GGAAGGCGAT TGTGGAAC
1201 GCAGATAGTC TGACGAAGTT CCGCCGACG TATATTATCA GTCGTGGAGG CTACATCGGT
1261 AATCAGCATT TTGGTGGGAT GTGGGTAGGA GACAACCTTT CTACGGGAAGA CTACCTCGCA
1321 ATGATGGTTA TCAACGTTAT CAACATGAAC ATGTCGGGTG TCCCCTCGT TGGTTCCGAT
1381 ATTGGAGGTT TCACGGAGCA TGACAAGAGA AACCCCTTGA CACCGGACTT GATGATGAGA
1441 TTTGTGACAG CTGGATGCTT GCTACCCTGG TTCAGGAACC ACTACGATAG GTGGATCGAG
1501 AGCAAGAAAC ACGGAAAGAA CTACCAAGAG TTGTACATGT ACCGCGACCA CTTGGACGCC
1561 TTAGAAGATT TTGTGGAAC CCGCTATCGC TGGCAGGAAG TGTATACAC AGCCATGTAT
1621 CAGAATGCTT TGAACGGGAA GCCGATCATC AAAACGGTCT CCATGTACAA CAACGATATG
1681 AACGTCAAAG ATGCTCAGAA TGACCACTTC CT
    
```

CLAIMS

1. A process of preparing a medium that comprises an anti-oxidant and at least one other component, the process comprising preparing *in situ* in the medium the anti-oxidant; and wherein the anti-oxidant is prepared from a glucan by use of recombinant DNA techniques.  
5
2. A process according to claim 1, wherein the glucan comprises  $\alpha$ -1,4 links.
- 10 3. A process according to claim 1 or claim 2 wherein the glucan is starch.
4. A process according to any one of the preceding claims wherein the glucan is a substrate for a recombinant enzyme such that contact of the glucan with the recombinant enzyme yields the anti-oxidant.  
15
5. A process according to any one of claims 1 to 4, wherein the enzyme is a glucan lyase.
6. A process according to claim 5, wherein the enzyme is an  $\alpha$ -1,4-glucan lyase.  
20
7. A process according to claim 6, wherein the enzyme comprises any one of the sequences shown as SEQ ID Nos 1-6, or a variant, homologue or fragment thereof.
8. A process according to claim 7, wherein the enzyme is any one of the sequences shown as SEQ ID Nos 1-6.  
25
9. A process according to any one of claims 5 to 8, wherein the enzyme is encoded by a nucleotide sequence comprising any one of the sequences shown as SEQ ID Nos 7-12, or a variant, homologue or fragment thereof.  
30
10. A process according to claim 9, wherein the enzyme is encoded by a nucleotide sequence having any one of the sequences shown as SEQ ID Nos 7-12.

11. A process according to any one of the preceding claims, wherein the anti-oxidant is anhydrofructose.
12. A process according to claim 11, wherein the anti-oxidant is 1,5-D-  
5 anhydrofructose.
13. A process according to any one of the preceding claims, wherein the medium is, or is used in the preparation of, a foodstuff.
- 10 14. A process according to claim 13, wherein the foodstuff is a beverage.
15. A process according to claim 14, wherein the beverage is an alcoholic beverage.
- 15 16. A process according to claim 14, wherein the beverage is a wine.
17. A process according to any one of the preceding claims, wherein the anti-oxidant is prepared *in situ* in the component and is then released into the medium.
- 20 18. A process according to any one of the preceding claims, wherein the component is a plant or a part thereof.
19. A process according to claim 18, wherein the component is all or part of a cereal or a fruit.
- 25 20. A process according to claim 20, wherein the component is all or part of a grape.
21. A process of preparing a medium that comprises an anti-oxidant and at least  
30 one other component, the process comprising preparing *in situ* in the medium the anti-oxidant; and wherein the anti-oxidant is prepared by use of a recombinant glucan lyase.

22. A process according to claim 21 wherein the glucan lyase is that as defined in any one of claims 6 to 10.
23. A medium prepared by the process according to any one of the preceding  
5 claims.
24. Use of anhydrofructose as an anti-oxidant for a medium comprising at least one other component, wherein the anhydrofructose is prepared *in situ* in the medium.
- 10 25. Use of anhydrofructose as a means for imparting or improving stress tolerance in a plant, wherein the anhydrofructose is prepared *in situ* in the plant.
26. Use of anhydrofructose as a means for imparting or improving the transformation of a grape, wherein the anhydrofructose is prepared *in situ* in the  
15 grape.
27. Use of glucan lyase as a means for imparting or improving stress tolerance in a plant, wherein the glucan lyase is prepared *in situ* in the plant.
- 20 28. Use of glucan lyase as a means for imparting or improving the transformation of a grape, wherein the glucan lyase is prepared *in situ* in the grape.
29. Use of a nucleotide sequence coding for a glucan lyase as a means for imparting or improving stress tolerance in a plant, wherein the nucleotide sequence  
25 is expressed *in situ* in the plant.
30. Use of a nucleotide sequence coding for a glucan lyase as a means for imparting or improving the transformation of a grape, wherein the nucleotide sequence is expressed *in situ* in the grape.  
30
31. A process or medium substantially as described herein.